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RESULT 1
US-11-087-528-4
; Sequence 4, Application US/11087528
; Publication No. US20050271664A1
; GENERAL INFORMATION:
; APPLICANT: JIAO, JIN-AN
; APPLICANT: WEN, JING HAI
; TITLE OF INVENTION: OF USE THEREOF
; FILE REFERENCE: TNA-065.06
; CURRENT FILING DATE: 2005-03-22
; PRIOR PAPLICATION NUMBER: 10/293,417
PRIOR FILING DATE: 2002-11-12
; PRIOR FILING DATE: 1999-04-16
; PRIOR FILING DATE: 1999-04-16
; PRIOR FILING DATE: 1997-03-10
; RUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 4
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Publication No. US20060039901A1
GENERAL INFORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
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31, Appli
32, Appli
143, Appli
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100.0%; Score 617; DB 7;
Best Local Similarity 99.1%; Pred. No. 5.9e-50;
Matches 116; Conservative 0; Mismatches 1;
US-11-097-812-144
US-11-097-812-145
US-11-17-567-204
US-11-180-187A-3
US-11-180-187A-3
US-11-165-023-31
US-11-097-812-138
US-11-097-812-134
US-11-097-812-144
US-11-202-507A-7
US-10-016-686-1
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  ORGANISM: Homo sapiens
  LENGTH: 117
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Sequence 39, 1
Sequence 5, Al
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617
1 BIQLQQSGPELVKPGASVQV......RDVTTALDFWGQGTTLITVSS 117
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1: /SIDS5/ptcdata/2/pubpaa/US08 NEW PUB.pep:*

2: /SIDS5/ptcdata/2/pubpaa/US07 NEW PUB.pep:*

3: /SIDS5/ptcdata/2/pubpaa/US07 NEW PUB.pep:*

4: /SIDS5/ptcdata/2/pubpaa/PCT NEW PUB.pep:*

5: /SIDS5/ptcdata/2/pubpaa/US10 NEW PUB.pep:*

6: /SIDS5/ptcdata/2/pubpaa/US10 NEW PUB.pep:*

7: /SIDS5/ptcdata/2/pubpaa/US10 NEW PUB.pep:*

8: /SIDS5/ptcdata/2/pubpaa/US11 NEW PUB.pep:*
                     GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-037-199-5
US-10-504-389A-26
US-11-07-812-72
US-11-097-812-81
US-11-097-812-81
US-11-097-812-64
US-11-097-812-65
US-11-097-812-65
US-11-097-812-67
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US-11-097-812-71
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US-11-097-812-206
US-11-097-812-136
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Maximum Match 100%
Listing first 45 summaries
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61 DONFKGKATLIVDKSSTTAFMHLNSLISDDSAVYFCAR---DVTTALDFWGQGTTLIVSS 117
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Sequence 6, Application US/10246019A

Publication No. US20060073133A1

GENERAL INFORMATION:

APPLICANT: Kikly, Kristine K.

APPLICANT: Abrahmson, Julie

TITLE OF INNENTION: Staloachesin Factor-3 Antibodies

FILE REFERENCE: GH50019-1C1

CURRENT PAPLICATION NUMBER: USSN 09/577,930

PRIOR APPLICATION NUMBER: USSN 09/577,930

PRIOR APPLICATION NUMBER: USSN 09/046,736

PRIOR PILING DATE: 1998-03-24

PRIOR PILING DATE: 1998-03-24

PRIOR PILING DATE: 1998-03-24

PRIOR PILING DATE: 1998-04-02

NUMBER FO SEQ ID NOS: 14

SOFTWARE: FRAESEQ for Windows Version 3.0

SEG ID NO 6
                                                                                                                                                                                                                                                                                                                                                                                                                           80.8%; Score 498.5; DB 7; 79.2%; Pred. No. 4.4e-39; atrive 11; Mismatches 11;
PRIOR FILING DATE: 2002-7-19
PRIOR APPLICATION NUMBER: JP 2002-211768
PRIOR PILING DATE: 2002-7-19
PRIOR PELING DATE: 2003-0-19
PRIOR APPLICATION NUMBER: JP 2003-051943
PRIOR APPLICATION NUMBER: JP 2003-198270
PRIOR PELING DATE: 2003-7-17
PRIOR APPLICATION NUMBER: JP 2003-198281
PRIOR PILING DATE: 2003-7-17
PRIOR APPLICATION NUMBER: JP 2003-198292
PRIOR FILING DATE: 2003-7-17
NUMBER OF SEQ ID NOS: 49
SOFTWARE: PATENTIN Ver: 2.1
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US-10-504-389A-28
; Sequence 28, Application US/10504389A
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Best Local Similarity 79.2*
Matches 95; Conservative
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US-11-037-199-5
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Matches 91, Conserv
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Publication No. US20060024302A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVENTION: CHIMERIC ANTI-VEGF-D ANTIBODIES AND HUMANIZED ANTI-VEGF-D ANTIBODITIE OF INVENTION: ADD METHODS OF USING SAME
FILE REPERENCE: 28967/339694
CURRENT APPLICATION NUMBER: US/11/074,373
CURRENT FILING DATE: 2005-03-07
NUMBER OF SEQ ID NOS: 52
SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NOS: 52
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                      FILE REFERENCE: 71758/46943-CIPZ.
CURRENT APPLICATION NUMBER: US/11/122,622
CURRENT FILING DATE: 2005-05-05
FRIOR APPLICATION NUMBER: US/09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 4
LENGTH: 117
TYPE: PRI
         TITLE OF INVENTION: OF USE THEREOF
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TYPE: PRT
ORGANISM: Homo sapiens
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Sequence 81, Application US/11097812
Sequence 81, Application US/20502818281
Sequence 81, Application No. US205020818281
Sequence 81, Application No. US205020818281
Septicant Norwarion
APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
APPLICANT: Bowdish, Katherine S.
TITLE OF INVENTION: BETROOF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS
TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING COURENT FILING DATE: 2004-10-1
PRIOR PILING DATE: 2004-10-1
PRIOR PELING DATE: 2004-10-28
PRIOR PELING DATE: 2004-03-04
PRIOR FILING DATE: 2004-03-04
PRIOR PILING DATE: 2003-12-15
PRIOR PELING DATE: 2003-12-15
PRIOR PELING DATE: 2003-03-04
PRIOR PILING DATE: 2003-03-04
PRIOR FILING DATE: 2003-03-04
NUMBER OF SEQ ID NOS: 207
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                                         62 NLKFKGKATILTVDKSSSTAYMOLNSLISEDSAVYYCGRSKRDYFDYWGOGTTLTVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ch 74.4%; Score 459; DB 7; Length 119; I Similarity 72.3%; Pred. No. 1.8e-35; 86; Conservative 16; Mismatches 15; Indels
                                                                                                                                                                            ; Sequence 72, Application US/11097812; Publication No. US20050281828A1; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                : PatentIn version 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; ORGANISM: mouse
US-11-097-812-72
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Best Local S:
Matches 86
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TITLE OF INVENTION: POLYPEPTIDES AND ANTIBODIES DERIVED FROM CHRONIC LYMPHOCYTIC LEUK
TITLE OF INVENTION: CELLS AND USES THEREOF
CURRENT FILING DATE: 2005-06-30
PRIOR APPLICATION NUMBER: US 10/996,316
PRIOR APPLICATION NUMBER: US 10/996,316
PRIOR FILING DATE: 2004-01-23
PRIOR FILING DATE: 2004-01-25
PRIOR FILING DATE: 2003-12-15
PRIOR FILING DATE: 2003-12-15
PRIOR FILING DATE: 2001-12-10
PRIOR FILING DATE: 2001-12-08
NUMBER OF SEQ ID NOS: 213
SOFTWARE: PATENTIN VERBION 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                        ; OTHER INFORMATION: amino acid sequence for murine 19/2 heavy chain variable region US-10-504-389A-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18 EVQLQQSGPELVKPGASVKISCKASGYTFTDYNIHWVKQSHGKSLDWIGYIAPYSGGTGY 77
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                                           APPLICANT: Rennet, Christoph
APPLICANT: Scott, Andrew
TITLE OF INVENTION: FUSION PROTEINS OF HUMANIZED G250 SPECIFIC
TITLE OF INVENTION: ANTIBODIES AND USES THEREOF
FILE REFERENCE: LUD 5821
CURRENT APPLICATION NUMBER: US/10/504,389A
CURRENT FILING DATE: 2004-08-10
PRIOR APPLICATION NUMBER: PCT/US03/04243
PRIOR FILING DATE: 2002-02-12
NUMBER OF SEQ ID NOS: 56
SEQ ID NO 28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                75.9%; Score 468.5; DB 6; Length 139; 73.7%; Pred. No. 2.9e-36; ive 15; Mismatches 15; Indels 1
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Publication No. US20060057651A1
GENERAL INFORMATION:
APPLICANT: Bowdish, Katherine S.
APPLICANT: McWhirter, John
Publication No. US20060045876A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 73.7%;
"...hes 87; Conservative
                                                                                                                                                                                                                                                                                                                       LENGTH: 139
TYPE: PRT
ORGANISM: Mus musculus
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Best Local Similarity
Matches 85; Conserv
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US-11-171-567-203
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LENGTH: 118
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Sequence 64, Application US/11097812

Sequence 64, Application US/11097812

Publication No. US20050281828A1

GENERAL INFORMATION:

APPLICANT: Bowdish, Katherine S.

APPLICANT: Bowdish, Ratherine S.

APPLICANT: Bowdish, Naveen

TITLE OF INVENTION: WEENDOOF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN

TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRICE OF INVENTION: WUMBER: US/11/097,812

CURRENT APPLICATION NUMBER: US 11/016,647

PRIOR APPLICATION NUMBER: US 11/016,647

PRIOR FILING DATE: 2004-03-04

PRIOR FILING DATE: 2004-03-04

PRIOR FILING DATE: 2004-03-04

PRIOR FILING DATE: 2003-03-04

PRIOR FILING DATE: 2003-03-12-15

PRIOR FILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US 60/529,500

PRIOR FILING DATE: 2003-12-15

PRIOR FILING DATE: 2003-12-15

PRIOR FILING DATE: 2003-03-04

PRIOR FILING DATE: 2003-12-15

PRIOR FILING DATE: 2003-12-15
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PRIOR APPLICATION NUMBER: US 11/016,647
PRIOR FILING DATE: 2004-12-17
PRIOR APPLICATION NUMBER: PCT/USO4/06570
PRIOR PLING DATE: 2004-03-04
PRIOR FILING DATE: 2004-02-28
PRIOR PRLING DATE: 2004-02-28
PRIOR PPLICATION NUMBER: US 60/529,500
PRIOR APPLICATION NUMBER: US 60/529,500
PRIOR PRIOR DATE: 2003-12-15
PRIOR PLING DATE: 2003-12-15
PRIOR PLING DATE: 2003-04
PRIOR PLING DATE: 2003-04
PRIOR PLING DATE: 2003-04
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US-11-097-812-64
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US-11-097-812-64
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SEQ ID NO 64
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APPLICANT: Dall'Acque, William
APPLICANT: Dall'Acque, William
APPLICANT: DameArcader, Melissa
TITLE OF INVENTION: INCREASING THE PRODUCTION OF RECOMBINANT ANTIBODIES IN MAWMALIAN
TITLE OF INVENTION: CELLS BY SITE-DIRECTED MUTAGENESIS
FILE REFERENCE: AF5700US
CURRENT APPLICATION NUMBER: US 60/583,184
PRIOR APPLICATION NUMBER: US 60/624,153
PRIOR APPLICATION NUMBER: US 60/624,153
PRIOR FILING DATE: 2004-06-25
PRIOR FILING DATE: 2004-06-25
SOFTWARE: PACENTING NUMBER: US 60/624,153
SOFTWARE: PACENTIN VERSION 3.3
SEQUENTING THE STATE OF SEQUENCE OF S
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Publication No. US20050281828A1
GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Exacts Rommel, Anke
APPLICANT: Dakapagari, Naveen
TITLE OF INVENTION: METHOD OF TREATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN
FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)
CURRENT APPLICATION NUMBER: US/11/097,812
CURRENT FILING DATE: 2005-04-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 NQKFKGKATLIVDKSSSTAYMQLKSLTSEDSAVYYCARTATALSTMDYWGQGTSVTVSS 119
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                                                                                                                                                                                                                                                               74.4%; Score 459; DB 7; Length 119; 72.3%; Pred. No. 1.8e-35; rive 16; Mismatches 15; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; Sequence 16, Application US/11165023
; Publication No. US20060019342A1
; GENERAL INFORMATION:
       SOFTWARE: PatentIn version 3.2 SEQ ID NO 81 LENGTH: 119 TYPE: PRT
                                                                                                                                                                                                                                                                                                                                           86; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: Artificial
                                                                                                                                                                                                                                                                                                         Best Local Similarity
Matches 86; Conserv
                                                                                                                                                        ; ORGANISM: mouse
US-11-097-812-81
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US-11-165-023-16
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                                                                                                                                                                                               Query Match

73.6%; Score 454; DB 7; Length 119;
Best Local Similarity 70.6%; Pred. No. 5.3e-35;
Matches 84; Conservative 15; Mismatches 18; Indels
                                                  ; ORGANISM: mouse
US-11-097-812-66
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US-11-097-812-67
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          RESULT 13
US-11-097-812-65

1 Sequence 65, Application US/11097812

2 Sequence 65, Application US/11097812

3 Sequence 65, Application US/11097812

3 GENERAL INFORMATION NO. US20050281828A1

3 APPLICANT: Bowdish, Katherine S.

4 APPLICANT: Bowdish, Katherine S.

5 APPLICANT: Wreat Formen, Ashe

7 TITLE OF INVENTION: WETSEN TO PERATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN

7 TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS

7 FILE REPRENCE: 100 PCT CIP II (1087-82 PT CIP II)

7 FILE PREPARENCE: 2004-04-04-04

7 FILE PRIOR APPLICATION NUMBER: PCT/US04/06570

7 PRIOR PELICATION NUMBER: PCT/US04/06570

7 PRIOR FILING DATE: 2004-02-28

7 PRIOR FILING DATE: 2004-02-28

7 PRIOR FILING DATE: 2004-02-38

7 PRIOR PILING DATE: 2003-12-15

7 PRIOR APPLICATION NUMBER: US 60/529,500

7 PRIOR APPLICATION NUMBER: US 60/529,500

7 PRIOR APPLICATION NUMBER: US 60/529,500

8 PRIOR PELING DATE: 2003-12-15

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8 PRIOR PELING DATE: 2003-12-15

9 PRIOR PELING DATE: 2003-12-15
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APPLICANT: Bowdish, Katherine S.

APPLICANT: Bowdish, Katherine S.

APPLICANT: Bowdish, Katherine S.

APPLICANT: Bratepagari, Maveen

TITLE OF INVENTION: METHOD OF TEATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN

TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CELLS

FILE REFERENCE: 100 PCT CIP II (1087-82 PCT CIP II)

CURRENT PPLICATION NUMBER: US/11/097,812

CURRENT FILING DATE: 2004-01

PRIOR APPLICATION NUMBER: PCT/US04/06570

PRIOR APPLICATION NUMBER: PCT/US04/06570

PRIOR PILING DATE: 2004-02-28

PRIOR PILING DATE: 2004-02-28

PRIOR PILING DATE: 2003-03-04

PRIOR FILING DATE: 2003-03-04

PRIOR FILING DATE: 2003-03-04

PRIOR FILING DATE: 2003-03-04

PRIOR PILING DATE: 2003-03-04

SOFTWARE: PACHOTION NUMBER: US 60/529,500

PRIOR PILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US 60/529,500

PRIOR PILING DATE: 2003-12-15

PRIOR PILING DATE: 2003-12-15

PRIOR PILING DATE: 2003-12-15

PRIOR PILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US 60/529,500

PRIOR PILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US 60/529,500

PRIOR APPLICATION NUMBER: US 60/529,500

PRIOR PILING DATE: 2003-12-15

PRIOR APPLICATION NUMBER: US 60/529,500

PRIOR APPLICATION NUMBER: US 60/529,500
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Publication No. US20050281828A1
GENERAL INFORMATION:
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Matches 85; Conservative
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US-11-097-812-66
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Sequence 67, Application US/11097812

Sequence 67, Application US/11097812

Sequence 67, Application No. US20050281828A1

SEDICANT: Bowdieb, Katherine S.

APPLICANT: Bowdieb, Katherine S.

APPLICANT: Bowdieb, Katherine S.

APPLICANT: Bowdieb, Katherine S.

TITLE OF INVENTION: METHOD OF TEATING AUTOIMMUNE DISEASE BY INDUCING ANTIGEN PRESENTING CELLS

TITLE OF INVENTION: PRESENTATION BY TOLERANCE INDUCING ANTIGEN PRESENTING CURRENT APPLICATION NUMBER: US/11/097,812

CURRENT FILING DATE: 2005-04-01

PRIOR APPLICATION NUMBER: US/11/097,812

CURRENT FILING DATE: 2004-12-17

PRIOR PILING DATE: 2004-02-28

PRIOR APPLICATION NUMBER: US 60/548,385

PRIOR PILING DATE: 2004-03-04

PRIOR APPLICATION NUMBER: US 60/529,500

PRIOR APPLICATION NUMBER: US 60/529,500

PRIOR FILING DATE: 2003-12-15

PRIOR PILING DATE: 2003-03-04

NUMBER OF SEQ ID NOS: 207

SOFTWARE: Patentin version 3.2

SEQ ID NO 67
61 DQNFKGKATLIYDKSSTTAFMHLNSLTSDDSAVYFCARDVTT--ALDFWGQGTTLIVSS 117
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Scoring table:

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The present sequence represents the human anti-tissue factor heavy chain variable region from an antibody that binds native human tissue factor (TF) and does not bind non-native TF. The antibody capable of specifically-binding-native TF. may, be used for inhibiting-blood coagulation and also for reducing-TF-levels in a mammal. The antibodies coagulation and also for reducing-TF-levels in a mammal. The antibodies restences to the thromboses-particularly to prevent or inhibit restences. Or other thromboses-particularly coprevent or inhibit settences as a treatial or cardiac surgery (e.g. angloplasty, endarterectomy, deployment of a stent, use of catheter, graft implantation or use of an
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AAY52755 AAY52756 ABR42727 ABR82930 ADI26469

Result ģ Anti-tiss Anti-huma Murine I4

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arteriovenous shunt). The antibodies can also be used as a carrier for drugs, particularly pharmaceuticals targeted for interaction with a blood clot such as streptokinase, tissue plasminogen activator (t-PA) or urokinase, or a cytotoxic agent by conjugating a suitable toxin to the antibody. Further the antibodies can be used for treating a thromboembolic condition associated with cardiovascular disease, an infectious disease, a neoplastic disease or as a thrombombolytic agent. The antibodies can also be used for detection and diagnosis
                                                                                                                                                                                                  1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                              9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is the protein sequence of the heavy chain variable
                                                                                                                                                                                                                                                      DONFKGKATLTVDKSSTTAFWHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                     New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coagulation or blood clot formation, angiogenesis, tumor metastases or
                                                                                                                                                                                                                       BIQLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                                                                          Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Tl89ue factor; antibody; H36.D2.B7; anticoagulant; cytostatic; antiinflammatory; mouse.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note= "complementarity determining region 3"
                                                                                                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region
                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      'note= "complementarity determining
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "apparently encoded by TATT
                                                                                                                                                                          ä
                                                                                                                                                Score 617; DB 2;
Pred. No. 4e-49;
                                                                                                                                                                                                                                                                                                                                                                                                                           Anti-tissue factor antibody H36.D2.B7 VH region.
                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mosquera LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                               ABR42700 standard; protein; 117 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 1; Fig 1B; 110pp; English
                                                                                                                                             100.0%;
99.1%; E
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               29-OCT-2001; 2001US-0343306P.
21-NOV-2001; 2001US-00990586.
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                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       inflammation in a mammal.
                                                                                                                                                                         Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2003-468399/44.
N-PSDB; ACC58569.
                                                                                                                                                              Best Local Similarity
                                                                                                                       Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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                                                                                                                                                 Query Match
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ABR42700
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        H36.D2.B7 (ATCC HB-12255). The invention relates to antibodies, especially humanized H36.D2.B7, that provide superior anticoagulant activity by binding native human TF with high affinity and specificity. The antibodies bind human TF, either alone or present in a TF:Factor VIIa complex, effectively preventing Factor X (or Factor IX) binding to TF or the complex, and thereby reducing blood coagulation. The humanized antibodies are useful for inhibiting blood coagulation or blood clot formation, anglogenesis, tumour metastases or inflammation in a mammal. They are also useful as drug carriers, as cytotxic agents, for reducing TF levels in mammals, and for in vivo diagnosis
                                                                                                                                                                                                                                                                    anti-recombinant human tissue factor (TF) murine antibody
                                                                                                                                                                                                                                                                                                                            DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                                                                     EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                                                                                                                          Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Tissue factor; humanization; antibody; anticoagulant; cytostatic;
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                                                                                                                                                                                              Length 117;
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                                                                                                                                                                                              Score 617; DB 6; Length 1
Pred. No. 4e-49;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Anti-tissue factor chimeric antibody cH36 VH region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          determining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "complementarity
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.98
re= "framework 3"
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|note= "framework 1"
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/note= "framework 4"
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21-NOV-2001; 2001US-00990586
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                                                                                                                                                                                                            99.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
                                                                                                                                                                                                                        Matches 116; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       antiinflammatory; mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note=
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                                                                                                                                                                                               Query Match
Best Local Similarity
                                                                                                                                                                   Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO2003037911-A2
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Region
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The present sequence is the protein sequence of the heavy chain variable region (VH) of anti-recombinant human tissue factor (TF) mouse-human chimeric antibody cH36. This sequence has been humanized in a series of steps (see ABR42719-34) to provide a humanized VH sequence for use in the production of an anti-human TF humanized antibody. Humanized antibodies of the invention provide superior anticoagulant activity by binding native human TF with high affinity and specificity. The antibodies bind human TF, either alone or present in a TF:Factor VIIa complex, effectively preventing Factor X (or Factor IX) binding to TF or the complex, and thereby reducing blood coagulation. The humanized antibodies are useful for inhibiting blood coagulation or blood clot formation, and inhibiting blood coagulation or blood clot formation, also useful as drug carriers, as cytotoxic agents, for reducing TF levels in mammals, and for in vivo diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       murine; mouse; humanised antibody; variable domain; framework region; FR; huFR; immune system molecule; H36.D2.B7; anti-tissue factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coagulation or blood clot formation, angiogenesis, tumor metastases or inflammation in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Murine anti-tissue factor heavy chain antibody protein SegID 4.
                                                                                                                                                                                                                                                                                                                                                                                                        DB 6; Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                   ; Score 617; DB 6; Length 11'
Pred. No. 4e-49;
0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Encoded by TCT"
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                                                                                Claim 12; Fig 13; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADL35005 standard; protein; 117
                                                                                                                                                                                                                                                                                                                                                                                                   100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 99.19
Matches 116; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                      Sequence 117 AA;
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Misc-difference
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Mosquera LA;

Stinson JR, 2004-239169/22.

Wong HC,

N-PSDB; ADL35004

SUNO-) SUNOL MOLECULAR CORP.

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This invention relates to a novel method for producing a humanised antibody variable (V) domain or its fragment by optimising sequence similarity between individual antibody framework regions (FRB) in order CC similarity between individual antibody framework regions (FRB) in order to identify suitable human FRS (huFRB). Specifically, it refers to novel immune system molecules i.e. humanised anonoclonal antibodies that exhibit suitable binding affinity with reduced immunogenicity in humans. The present invention describes a method of mutagenising DNA of non-human FRB CC substantially identical to the selected human FR previously identified controlly sequence similarity searching. As such, this method provides CC humanised light or heavy chain V domains of the sequence huRRI-CDRI-huFR2 CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic controlly incomined or diagnostic controlly incomined the number of best fit possibilities that CC an be generated and provides a rational basis for assembling nearly all humanised immune system molecules of interest. This polypeptide sequence CC is a mutrine anti-tissue factor heavy chain antibody H36.D2.B7 protein of
regions to help identify human framework regions suitable for making the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          septic shock syndrome; tissue factor; antibacterial; immunosuppressive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DQNFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLIVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0; · Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                               99.8%; Score 616; DB 8; Length 117;
100.0%; Pred. No. 5e-49;
ive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Variable amino acid"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Murine H36.D2.B7 antibody VH SEQ ID NO:4.
                                               Disclosure; SEQ ID NO 4; 137pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note= "Encoded by TCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
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/label= CDR2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-JAN-2004; 2004US-00764140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97US-00814806
99US-00293854
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99. .106
/label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /label= CDR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibody; antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local Similarity 100.'
Matches 117; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 117 AA;
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Misc-difference
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16-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Producing humanized antibodies for diagnostic and therapeutic purposes comprises optimizing similarity between individual antibody framework
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04-JUN-2004; 2004WO-US017900.

(SUNO-) SUNOL MOLECULAR CORP.

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19-JUN-2003; 2003US-0480254P. 22-JAN-2004; 2004US-0538892P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                   emptic shock syndrome in a manual, involving administering to the mammal and deeb not substantially bind non-native tissue factor. Where the factor x binding to the complex is inhibited and the administration is sufficient to prevent or treat the septic shock syndrome in the mammal. In (M1), the antibody has the binding specificity for native human tissue factor about equal to or greater than H36.D2.B7 (ATCC HB-12255), and is a monoclonal chimeric antibody. An antibody of the invention has antibacterial and immunosuppressive activity, and acts as an inhibitor of binding persent sequence represents the heavy chain variable region of the murine antibody of the invention, H36.D2.B7 (ATCC HB-12255).
                                                                                                                                                                            Treating or preventing septic shock syndrome in mammal, involves administering antibody that binds native human tissue factor and does not substantially bind non-native tissue factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                       The invention relates to a novel method for treating or preventing (M1)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 DONFKGKATLITVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLIVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               antinflammatory, antibody, tissue factor; sepsis; disseminated intravascular coagulation; anticoagulant; hematological disease; thrombosis; lung injury; respiratory-gen.; respiratory distress syndrome; Immunosuppressive; Antibacterial; Antianthritic; Antianemic; anemia; rheumatoid arthritis; glomerulonephritis; multiple sclerosis; psoriasis; sjogren's syndrome; inflammatory bowel disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DONFKGKATLITVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLITVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 99.8%; Score 616; DB 8; Length 117;
100.0%; Pred. No. 5e-49;
iive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Blood-clotting; heavy chain variable region; inflammation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mouse anti-tissue factor antibody H36.D2.B7 VH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note= "Encoded by TCT"
                                                                                                                                                                                                                                                               Claim 44; SEQ ID NO 4; 28pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADW07328 standard; protein; 117 AA.
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12-NOV-2002; 2002US-00293417
                                        (SUNO-) SUNOL MOLECULAR CORP
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Matches 117; Conservative
                                                                                                                    WPI; 2004-813246/80.
N-PSDB; ADU06809.
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                                                                              Jiao J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2005004793-A2
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                                                                              Wong HC,
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ADW07328
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ઠે a ઠે 셤 20-JAN-2005

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The invention relates to preventing or treating a sepsis or inflammatory disease in a mammal comprising administering to the mammal a therapeutic disease in a mammal comprising administering to the mammal a therapeutic amount of at least one humanized antibody, chimeric antibody, or their fragment that binds specifically to tissue factor (TF) to form a complex, where factor X or IX binding to the complex is inhibited and the complex, administration prevents or treats the sepsis in the mammal. Also included are a kit for performing the above method and reducing an inflammatory cytokine production in a mammal. The inflammatory disease is associated are hirtis (preferably rheumatoid arthritis), glomerulonophritis, multiple sclerosis, psoriasis, Sjogren's syndrome, or inflammatory bowel disease. The method also treats or prevents a sepsis-related condition in a mammal, where the sepsis-related condition is an amammal, where the sepsis-related condition is an amammal, where the sepsis-related condition (s spois-related condition) or sepsis-related condition (c real disorder. The lung injury is acute lung injury (ALI) or acute c respiratory distress syndrome (ARDS). The sepsis-associated renal disorder the acute tubular necrosis. The methods and kit are useful for preventing or treating sepsis or sepsis-related conditions (e.g. DIC or anemia) or inflammatory diseases (e.g. arthritis). The humanized anemia or inflammatory diseases (e.g. arthritis). The humanized conthe chimeric antibody cuis which comprises the light and heavy chain variable regions (VL or VH) of an anti-TF antibody (sused to the human IgG4 heavy and kappa light constant regions. The CDRs (complementarity determining region) and FRS (framework regions) are then the humanized. The presente sequence represente the light or heavy chain without will be not be humanized. The presente the light by or heavy chain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9
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                                                                                                                                                                              Preventing or treating sepsis or inflammation in mammals comprises administering a humanized or chimeric antibody that binds to a human tissue factor to form a complex in which factor X or IX binding to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQCTTLTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        .
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100.0%; Pred. No. 5e-49;
tive 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      H36.D2.B7 anti-tissue factor heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; SEQ ID NO 4; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADZ40939 standard; protein; 117 AA
Egan JO;
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                                                                                                                                                                                                                                                                                                         complex is inhibited
                                                                   WPI; 2005-091964/10.
N-PSDB; ADW07327.
Wong HC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 117 AA;
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Jiao J,
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DONFKGKATLTVDKSSTTAFMHINSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117

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Tissue factor; humanization; antibody; anticoagulant; cytostatic; antiinflammatory; mouse.

Anti-tissue factor humanized antibody VH region HC-01.

(first entry)

26-AUG-2003

ABR42719;

ABR42719 standard; protein; 117 AA.

ABR42719

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The inversion relates to an antibody (I) that binds native human tissue factor and does not substantially bind non-native tissue factor. Also described: (1) an isolated nucleic acid (II) comprising a sequence encoding at least a portion of an antibody that binds native human tissue factor; (2) a recombinant vector (IV) comprising (II), where (IV) can express at least a portion of an antibody that binds native human tissue factor; (3) a host cell (V) comprising (IV); (4) inhibiting (MI) blood coagulation in a mammal by administering the antibody where the antibody complexes with native tissue factor and factor X binding to the complex is inhibited; (5) reducing (M2) tissue factor levels in a mammal by administering the antibody cowalently linked to a cell toxin or to an effector molecule to provide complement-fixing ability and antibody dependent cell-mediated cytotoxicity, where the antibody contacts cells axpressing the sample with the antibody (I), where the antibody is and (6) detecting (M3) tissue factor levels in a mammal; and (6) detecting the sample with the antibody (I), where the antibody is contacting the sample with the antibody (I), where the antibody is monoclonal. (I) is useful for inhibiting blood coagulation in a mammal (preferrably human), for reducing tissue factor levels in a mammal, contacting tissue factor in a biological sample. (I) can be used in the treatment of a thromboembolic condition associated with cardinatise factor and decoration as thrombosis and restenosis. The antibodies of the invention (especially H36.D2.B7 (secreted by hybridoma ATCC HB-12255)) bind strongly to a conformation of factor X to its activated form factor has the present sequence represents the H36.D2.B7 anti-tissue factor heaver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                invention relates to an antibody (I) that binds native human tissue
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibodies binding to native human tissue factor without substantial binding to non-native tissue factor, useful for inhibiting blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                coagulation, for reducing tissue factor, useful for inhibiting blood detecting tissue factor levels in a mammal, and for detecting tissue factor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 99.8%; Score 616; DB 9; Length 11 Best Local Similarity 100.0%; Pred. No. 5e-49; Matches 117; Conservative 0; Mismatches 0; Indels
                                                                                                                           /label= unkown
/note= "encoded by TCT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Claim 12; SEQ ID NO 4; 36pp; English.
                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                 11-JUL-2003; 2003US-00618338.
                                                                                                                                                                                                                                                                                                                                               16-APR-1999; 99US-00293854
12-NOV-2002; 2002US-00293417
                                                                                                                                                                                                                                                                                                                                                                                                                   (SUNO-) SUNOL MOLECULAR CORP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy chain variable region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2005-344279/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Wong HC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; ADZ40938.
                                                                                                        Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 117 AA;
                                                                                                                                                                                               US2005089929-A1
                                                                                                                                                                                                                                                                                                                          10-MAR-1997;
                      Ното варіепв
                                                                                                                                                                                                                                        28-APR-2005
                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jiao J,
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The present sequence is the protein sequence of a humanized version, HC-01, of the heavy chain variable region (VH) of anti-recombinant human tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR mutagenesis steps was used to introduce mutations into the cH36 sequence to fully humanize the VH region (see ABR42719-31) and hence for the production of an anti-human TF humanized antibody. Humanized antibodies of the invention provide superior anticoagulant activity by binding native human TF with high affinity and specificity. The antibodies bind human TF, either alone or present in a TF:Ractor VIIa complex, effectively preventing Factor X (or Factor IX) binding to TF or the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coagulation or blood clot formation, angiogenesis, tumor metastases or
                                                                                                                                                                                                                                                 .35
.e= "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                 "complementarity determining region 2"
                                                                                                                                                                                                                                                                                                                                                                    /note= "complementarity determining region 3"
                                                                                                                                                                                                                                     note= "wild-type Glu substituted by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "wild-type Leu substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mosquera LA;
                                                                                                                                                                                                                                                                                                                          .98
-e= "framework 3"
                                                                                                                                                                                                  l. .30
/note= "framework 1"
                                                                                                                                                                                                                                                                                       "framework 2"
                                                                                                                                                                                                                                                                                                                                                                                              'note= "framework 4"
                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Wong HC, Nieves EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-OCT-2002; 2002WO-US034727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2001; 2001US-0343306P.
21-NOV-2001; 2001US-00990586.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (SUNO-) SUNOL MOLECULAR CORP.
                                                                                                                                                                                                                                                                                                                                                       .106
                                                                                                                                                                                                                                                                                                                                                                                 .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    inflammation in a mammal.
                                                                                                                                                                                                                                                                           36. .49
                                                                                                                                                                                                                                                                                                     99.
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                                                                                                                                                                                                                                                                                                                                                                                 107
                                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                WO2003037911-A2.
                                                                                                                                                                                                                         Misc-difference
                                                                                                                               Mus sp.
Homo sapiens.
Chimeric.
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0; Gaps

Length 117;

61 DONFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117 1 BIQLQQSGPBLVKPGASVQVSCKTXGYSFTDYNVY#VRQSHGKSLEMIGYIDPYNGITIY 1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY

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complex, and thereby reducing blood coagulation. The humanized antibodies are useful for inhibiting blood coagulation or blood clot formation, anglogenesis, tumnur metastesses or infilammation in a mammal. They are also useful as drug carriers, as cytotoxic agents, for reducing TF levels in mammals, and for in vivo diagnosis
                                                                                              1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                             DONFKGKATLITVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                    Gaps
                                                                                                                                                                                                                                                humanization; antibody; anticoagulant; cytostatic;
                                                                              ;
                                                                                                                                                                                                                                                                                                                                                   "complementarity determining region 1"
                                                                                                                                                                                                                                                                                                                                                                                                                5
                                                               Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                  region
                                                                                                                                                                                                                                                                                                                                    note= "wild-type Glu substituted by Gln"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       113
/note= "wild-type Leu substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                notes "wild-type Ser substituted by Gly"
                                                                                                                                                                                                                                                                                                                                                                                 note= "wild-type His substituted by Pro"
                                                                                                                                                                                                                                Anti-tissue factor humanized antibody VH region HC-02.
                                                                                                                                                                                                                                                                                                                                                                                                       .66
:e= "complementarity determining
                                                              Score 611; DB 6;
Pred. No. 1.4e-48;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                'note= "complementarity
                                                                                                                                                                                                                                                                                                                                                                                                                     .98
-e= "framework 3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               'note= "framework 4"
                                                                                                                                                                                                                                                                                                                                                                  'note= "framework 2"
                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                  ABR42720 standard; protein; 117 AA.
                                                                                                                                                                                                                                                       antiinflammatory; human; mouse.
                                                             Query Match 99.0%;
Best Local Similarity 97.4%;
Matches 114; Conservative 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           29-OCT-2002; 2002WO-US034727
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          29-OCT-2001; 2001US-0343306P.
21-NOV-2001; 2001US-00990586.
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                                                                                                                                                                                                                 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                 'note=
                                                Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                         Misc-difference
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                                                                                                                                                                                                                                                factor;
                                                                                                                                                                                                                                                                      Mus sp.
Homo sapiens.
Chimeric.
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                                                                                                                                                                                                  ABR42720;
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The present sequence is the protein sequence of a humanized version, HC-
02, of the heavy chain variable region (VH) of anti-recombinant human
11ssue factor (FF) mouse-human chimeric antibody CH36. A series of PCR
mutagenesis steps was used to introduce mutations into the CH36 sequence
12 to fully humanize the VH region (see ABR42719-31) and hence for the
13 production of an anti-human FF humanized antibodie antibodies
14 of the invention provide superior anticoagulant activity by binding
15 cative human TF with high affinity and specificity. The antibodies bind
16 numan TF, either alone or present in a TF:Rector VIIs complex,
17 effectively preventing Factor X (or Factor IX) binding to TF or the
18 complex, and thereby reducing blood coagulation. The humanized antibodies
18 are useful for inhibiting blood coagulation or blood clot formation,
29 are useful so inhibiting so are inflammation in a mammal. They are
20 also useful as drug carriers, as cytotoxic agents, for reducing TF levels
20 in mammals, and for in vivo diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                              New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coaqulation or blood clot formation, angiogenesis, tumor metastases or inflammation in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          antibody; anticoagulant; cytostatic;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-tissue factor humanized antibody VH region HC-03.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 597; DB 6;
Pred. No. 2.8e-47;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               96.8%; Scor.
95.7%; Pred. No. 4..
2; Mismatches
  Mosquera LA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note= "framework 1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABR42721 standard; protein; 117 AA.
                                                                                                                                                                                                                                                           Claim 12; Fig 13; 110pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     antiinflammatory; mouse; human.
Nieves EL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tissue factor; humanization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31. .35
/note= "c
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                                                        WPI; 2003-468399/44.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference
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Homo sapiens.
Chimeric.
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Tissue factor; humanization; antibody; anticoagulant; cytostatic; antiinflammatory; mouse; human.

Anti-tissue factor humanized antibody VH region HC-04.

(first entry)

26-AUG-2003

ABR42722:

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The present sequence is the protein sequence of a humanized version, HC-
103. of the heavy chain variable region (VH) of anti-recombinant human
tissue factor (TF) mouse-human chimeric antibody CH36. A series of PCR
mutagenesis steps was used tro introduce mutations into the CH36 sequence
to fully humanize the VH region (see ABR42719-31) and hence for the
production of an anti-human TF humanized antibody. Humanized antibodies
of the invention provide superior anticoagulant activity by binding
native human TF with high affinity and specificity. The antibodies bind
numan TF, either alone or present in a TF:Factor VIIa complex,
effectively preventing Factor X (or Factor IX) binding to TF or the
complex, and thereby reducing blood coagulation. The humanized antibodies
are useful for inhibiting blood coagulation or blood clot formation,
angiogenesis, tumour metaetases or inflammation in a mammal. They are
also useful as drug carriers, as cyctoxic agents, for reducing TF levels
in mammals, and for in vivo diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coagulation or blood clot formation, angiogenesis, tumor metastases or
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                                                                                                                                                                             /note= "complementarity determining region 3"
 "complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         94.7%; Score 584; DB 6; Length 117; llarity 93.2%; Pred. No. 4.4e-46; Conservative 4; Mismatches 4; Indels
                                                                                                     note= "wild-type Asp substituted by Glu"
                                                                                                                                                                                                                                                  /note= "wild-type Leu substituted by Val"
                                                                  /note= "wild-type Thr substituted by
                                                                                                                                            ά
                                                                                                                                            Ser substituted
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                67. .98
/note= "framework 3"
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                                                                                                                                          'note= "wild-type
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig 13; 110pp; English.
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                                                                                                                                                                                            107. .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation in a mammal.
                                                                                                                                                               99. .106
   note=
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Best Local Similarity
Matches 109; Conserv
                                                                                     Misc-difference 89
                                                     Misc-difference
                                                                                                                                                                                                                               Misc-difference
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                  Region
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The present sequence is the protein sequence of a humanized version, HC-d4, of the heavy chain variable region (WH) of anti-recombinant human tissue factor (TF) mouse-human chimeric antibody cH36. A series of PCR mutagenesis steps was used to introduce mutations into the CH36 sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coagulation or blood clot formation, anglogenesis, tumor metastases or
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/note= "complementarity determining region

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    note= "complementarity determining region
107. .117

                                                                                                                                                                                             'note= "wild-type Glu substituted by Gln"
                                                                                                                                                                                                                                                                                                                                                         note= "wild-type His substituted by Glu"
                                                                                                                                                                                                                                                                                                                                                                                note= "wild-type Asn substituted by Ser"
                                                                                                                                                                                                                                                                                                                                                                                                     'note= "wild-type Thr substituted by Arg"
                                                                                                                                                                                                                                                                                                                                                                                                                            'note= "wild-type Asp substituted by Glu"
                                                                                                                                                                                                                                                               note= "wild-type His substituted by Pro"
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                                                                                                                                                                                                                                                                                                                                  note= "framework 3"
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/note= "framework 2"
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                                                                                                                                                 Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      inflammation in a mammal
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                                                                                                                                                                                                                    /note=
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                                                                                                                                                                                                                                                                           Misc-difference 44
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                                                                                                    Mus sp.
Homo sapiens.
Chimeric.
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Gaps . 0 61

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ABR42722 standard; protein; 117 AA.

RESULT 11 ABR42722 ID ABR4 XX

1 QIQLQQSGPELVKPGASVQVSCKTSGXSFTDYNVYWVRQSPGKGLEWIGYIDPYNGITIY 1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY

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Misc-difference 89

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                   production of an anti-human TF humanized antibody. Humanized antibodies of the invention provide superior anticoagulant activity by binding native human TF with high affinity and specificity. The antibodies bind human TF, either alone or present in a FFFEctor VIIa complex, effectively preventing Factor X (or Factor IX) binding to TF or the complex, and thereby reducing blood coagulation. The humanized antibodies are useful for inhibiting blood coagulation or blood clot formation, angiogenesis, tumour metastases or inflammation in a mammal. They are also useful as drug carriers, as cytocoxic agents, for reducing TF levels in mammals, and for in vivo diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DONFKGKATLTVDKSSTTAFMELSSLRSEDTAVYFCARDVTTALDFWGQGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01QLQQSGPELVKPGASVQVSCKTSGYSFTDYNVYWVRQSPGKGLEWIGYIDPYNGITIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0; Gaps
   fully humanize the VH region (see ABR42719-31) and hence for the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Tissue factor; humanization; antibody; anticoagulant; cytostatic;

    .35
    note= "complementarity determining region 1"

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92.5%; Score 571; DB 6; Length 117;
Best Local Similarity 91.5%; Pred. No. 7e-45;
Matches 107; Conservative 5; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  notes "wild-type Thr substituted by Ser"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 note= "wild-type Ser substituted by Gly"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Anti-tissue factor humanized antibody VH region HC-05
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Misc-difference 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Misc-difference 87
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 117 AA;
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Homo sapiens.
Chimeric.
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The present sequence is the protein sequence of a humanized version, HC-
05, of the heavy chain variable region (VH) of anti-recombinant human
citisue factor (FF) mouse-human chimeric antibody cH36. A series of PCR
mutagenesis steps was used to introduce mutations into the cH36 sequence
to fully humanize the VH region (see ABR42719-31) and hence for the
production of an anti-human FF humanized antibodise of the invention provide superior anticoagulant activity by binding
native human TF with high affinity and specificity. The antibodies bind
native human TF, either alone or present in a TF-Fractor VIIs complex,
effectively preventing Factor X (or Factor IX) binding to TF or the
complex, and thereby reducing blood coagulation. The humanized antibodies
are useful for inhibiting blood coagulation or blood clot formation,
are useful to inhibiting blood coagulation or blood clot formation,
angiquenesis, tumour metastases or inflammation in a mammal. They are
the mammals, and for in vivo diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                        New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coagulation or blood clot formation, angiogenesis, tumor metastases or inflammation in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DONFKGKATLIVDKSSTIAFMHLNSLISDDSAVYFCARDVTTALDFWGQGTTLIVSS 117
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                                                                  /note= "complementarity determining region 3" 107.\ .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 117;
               note= "wild-type Asp substituted by Glu"
                                               /note= "wild-type Ser substituted by Thr"
                                                                                                                                                   /note= "wild-type Leu substituted by Val"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 561, DB 6; Length 11
Pred. No. 5.8e-44;
8; Mismatches 5; Indels
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                                                                                                                                                                                                                                                                                                                                                                        Nieves EL, Mosquera LA;
                                                                                                                /note= "framework 4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Claim 12; Fig 13; 110pp; English
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                                                                                                                                                                                                                                                                                      29-OCT-2001; 2001US-0343306P.
21-NOV-2001; 2001US-00990586.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                 .106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
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                                                                                                                                   Misc-difference 113
                                                                                                                                                                                                                                                                                                                                                                      Wong HC,
                                 Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 117 AA;
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                                                                  Region
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New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coagulation or blood clot formation, angiogenesis, tumor metastases or inflammation in a mammal.
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         Tissue factor; humanization; antibody; anticoagulant; cytostatic; antiinflammatory; mouse; human.
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/note= "complementarity determining region 2"
                                                                                                                                                                                                                                                                    31. .35
/note= "complementarity determining region 1"
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(07. .117
                                                                                                                                                                 note= "wild-type Glu substituted by Gln"
                                                                                                                                                                                                                           'note= "wild-type Gln substituted by Arg"
                                                                                                                                                                                                                                                      note= "wild-type Thr substituted by Ala"
                                                                                                                                                                                                                                                                                                                                            'note= "wild-type His substituted by Pro"
                                                                                                                                                                                                                                                                                                                                                                       note= "wild-type Ser substituted by Gly"
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/note= "framework 1"
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67. .98
/note= "framework 3"
                                                                                                                                                                                                                                                                                               36. .49
/note= "framework 2"
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                                                                                                            Location/Qualifiers
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                                                                Homo sapiens
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The present sequence is the protein sequence of a humanized version, HC-
CO 9, of the heavy chain variable region (VH) of anti-recombinant human
tissue factor (TF) mouse-human chimeric antibody CH36. A series of PCR
mutagenesis steps was used to introduce mutations into the cH36 sequence
to fully humanize the VH region (see ABR42719-31) and hence for the
production of an anti-human TF humanized antibody. Humanized antibodies
of the invention provide superior anticosquiant activity by binding
native human TF with high affinity and specificity. The antibodies bind
numan TF, either alone or present in a TF:Ractor VIIa complex,
effectively preventing Factor X (or Factor IX) binding to TF or the
complex, and thereby reducing blood coagulation. The humanized antibodies
are useful for inhibiting blood coagulation or blood clot formation,
are useful so timbuse the mammal of the mammal. They are
also useful as drug carriers, as cytotoxic agents, for reducing TF levels
in mammals, and for in vivo diagnosis
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31. .35
/note= "complementarity determining region 1"
36. 49
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                                                                                                                                                                                                                                                                                                                                                                                                            Query Match 88.3%; Score 545; DB 6; Length 117; Best Local Similarity 86.3%; Pred. No. 1.7e-42; Matches 101; Conservative 9; Mismatches 7; Indels
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Claim 12; Fig 13; 110pp; English.
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                                                                                                                                                                                                                                                                                                                                                                      Sequence 117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus sp.
Hono sapiens.
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Region Region

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等於 內本 海馬

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New humanized antibody that binds specifically to human tissue factor, useful for in vivo diagnostic methods, or for inhibiting blood coagulation or blood clot formation, angiogenesis, tumor metastases or
                                                                                                                                                                         99. .106
/note= "complementarity determining region 3"
                                                                                                    'note= "wild-type Asn substituted by Ser"
                                                                                                                                                                                                                                                 /note= "wild-type Leu substituted by Val"
                  note= "wild-type Ser substituted by Thr"
                                                                                note= "wild-type His substituted by Glu"
                                                                                                                        note= "wild-type Thr substituted by Arg"
                                                                                                                                            note= "wild-type Asp substituted by Glu"
                                                                                                                                                                 note= "wild-type Ser substituted by Thr"
                                                                                                                                                                                                                             note= "wild-type Leu substituted by Val"
                                                           note= "wild-type Phe substituted by
                                         substituted
                                                                                                                                                                                                                                                                                                                                                                                      Mosquera LA;
                                      'note= "wild-type Thr
                                                                                                                                                                                                         'note= "framework 4"
"framework 3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 12; Fig 13; 110pp; English.
                                                                                                                                                                                                                                                                                                                                                                                     Wong HC, Nieves EL,
                                                                                                                                                                                                                                                                                                              29-OCT-2002; 2002WO-US034727
                                                                                                                                                                                                                                                                                                                                  29-OCT-2001; 2001US-0343306P.
21-NOV-2001; 2001US-00990586
                                                                                                                                                                                                                                                                                                                                                                 (SUNO-) SUNOL MOLECULAR CORP
                                                                                                                                                                                                .117
                                                                                                                                                                                                                                                                                                                                                                                                                                                            inflammation in a mammal
  /note=
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                                                                                                                                                                                                                                      Misc-difference 115
          Misc-difference
                             Misc-difference
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                                                                                                                                                                                                                                                                      WO2003037911-A2
                                                                                                                                                                                                                                                                                          08-MAY-2003
                                                                                                                                                                                                                                                                                                                                                                                    Jiao J,
                                                                                                                                                                           Region
                                                                                                                                                                                                Region
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The present sequence is the protein sequence of a humanized version, HC10, of the heavy chain variable region (WH) of anti-recombinant human
10, of the heavy chain variable region (WH) of anti-recombinant human
10, of the heavy chain variable region (WH) of anti-recombinant human
10, of the invention provide superior anticode mitabody when care for the
11 production of an anti-human TF humanized antibody. Mumanized antibodies
12 production of an anti-human TF humanized antibodies
13 cative human TF with high affinity and specificity. The antibodies bind
14 human TF, either alone or present in a TF:Factor VIIa complex,
15 caffectively preventing Factor X (or Factor IX) binding to TF or the
16 complex, and thereby reducing blood coagulation. The humanized antibodies
16 are useful for inhibiting blood coagulation or blood clot formation,
17 cangiogenesis tumour metastases or inflammation in a mammal. They are
18 also useful as drug carriers, as Cytotoxic agents, for reducing TF levels
18 in mammals, and for in vivo diagnosis

1 OIOLVOSGPEVVKPGASVRVSCKASGXSFTDYNVYWVROSPGKGLEWIGYIDPYNGITIY 1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 87.8%; Score 542; DB 6; Length 11.85.5%; Pred. No. 3.3e-42; 7; Indels Best Local Similarity 85.5 Matches 100; Conservative Query Match Best Local S

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ö 9 9

Gaps ö

Length 117;

117 DONFKGKATLITVDKSTSTAYMELSSLRSEDTAVYFCARDVTTALDFWGQGTTVTVSS 117 DONFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS Tissue factor; humanization; antibody; anticoagulant; cytostatic; antiinflammatory; mouse; human. ٦, 2 note= "complementarity determining region 3" . .66
 'note= "complementarity determining region "complementarity determining region Glu" note= "wild-type Ile substituted by Met" note= "wild-type Glu substituted by Gln" Arg" Arg" /note= "wild-type Leu substituted by Val" 'note= "wild-type His substituted by Pro" note= "wild-type Thr substituted by Ser" note= "wild-type Ser substituted by Thr" Anti-tissue factor humanized antibody VH region HC-06. ά 'note= "wild-type Gln substituted by 'note= "wild-type Thr substituted by 'note= "wild-type Ser substituted by note= "wild-type Phe substituted by notes "wild-type His substituted by note= "wild-type Asn substituted by 'note= "wild-type Asp substituted by note= "wild-type Ser substituted by 'note= "wild-type Thr substituted 'note= "wild-type Pro substituted 36. .49 /note= "framework 2" 57. .98 'note= "framework 3" 1. .30
/note= "framework 1" note= "framework 4" Location/Qualifiers protein; 117 AA (first entry) 99. .106 note= ABR42724 standard; Misc-difference 19 Misc-difference 24 Misc-difference 41 Misc-difference 82 Misc-difference 87 Misc-difference 7 Misc-difference WO2003037911-A2 sp. o sapiens. 26-AUG-2003 61 ABR42724; 61 Chimeric Region Region Region Region Region Region Region Homo Mus Key ઠે 셤

 Query Match
 87.5%;
 Score 540;
 DB 6;
 Length 117;

 Best Local Similarity
 85.5%;
 Pred. No. 5e-42;
 Antches 100;
 Conservative 10;
 Mismatches 7;
 Indels 0;
 Gaps 0

 Qy
 1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
 ::|||||||||||||||||
 Db
 1 QMQLQQSGGELVKPGASVRSCKASGYSFTDYNVYWVRQSPGKGLEWIGYIDPYNGITIY 60

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Search completed: April 18, 2006, 13:35:38 Job time : 190 secs

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Sequence Sequence Sequence Sequence Sequence Sequence

Sequence Sequence Sequence

Sequence

Sequence Sequence Sequence Sequence

2, A 18,

Sequence Sequence Sequence 3

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APPLICANT: Word, Hing C.
APPLICANT: Word, Jin-an
APPLICANT: Jiao, Jin-an
APPLICANT: Esperanza, Nieves
APPLICANT: Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
          US-08-436-717-27
US-08-48-537-69
US-08-48-537-69
US-09-214-095D-14
US-09-94-0727B-14
US-09-312-157-14
US-09-312-157-14
US-09-312-157-14
US-09-301-593-30
US-09-301-593-30
US-10-114-716A-46
US-08-672-345C-16
US-09-246-095D-16
US-09-246-095D-16
US-09-246-095D-16
US-09-246-095D-16
US-09-486-814A-2
                                                                                                                                                                                                                                                            ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION WUBBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELEPHONE: 617-523-3400
TELEFAX: 617-523-3400
                                                                                                                                                                                                                                                                                                                          Sequence 4, Application US/08814806
Patent No. 5986065
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: peptide HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               linear
 USA
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STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: US
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                                                                                                                                                                                                                                                                                                               US-08-814-806-4
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 Sequence 4, Appli
Sequence 139, Appl
Sequence 140, App
Sequence 140, App
Sequence 153, App
Sequence 154, App
Sequence 55, Appl
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Appl
Appl
                                                                                April 18, 2006, 13:39:50 ; Search time 47 Seconds (without alignments) 205.810 Million cell updates/sec
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         GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
                                                                                                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/1/iaa/s_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6_COMB.pep:*
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US-09-647-468-130

US-09-647-468-140

US-09-647-468-153

US-09-647-468-154

US-09-647-468-154

US-09-647-468-154

US-09-647-468-144

US-09-647-468-144

US-09-214-095D-90

US-09-214-095D-90

US-09-214-095D-90

US-09-214-095D-90

US-09-247-468-157

US-09-647-468-157

US-08-65-906-25

US-08-673-345C-106

US-08-673-345C-106

US-08-673-345C-106
                                                                                                                                                                                                                                                     Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -08-474-040-69
-08-487-200-69
                                                                                                                                                                                                                              572060 segs, 82675679 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUMMARIES
                                                          OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                       Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
                                                                                                                                                                                                                                                                                                                                                                            Issued_Patents_AA:*
                                                                                                                                                                                                                                                                                Minimum DB seq length: 0
Maximum DB seq length: 200000000
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617
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Match Length
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TYPE: PRT
ORGANISM: Mus sp.
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US-09-647-468-139
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                                                                                                                                                                                                                        61 DONFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLIVSS 117
                                                                                                                                                                                                                                            61 DONFKGKATLITUDKSSTTAFMHINSLTSDDSAVYFCARDVTTALDFWGQGTTLITVSS 117
                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
STATE: MA
                                         Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 117;
                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Esperanza, Nieves
Lawrence, Luepechen
TITLE OF INVENTION: AND METHODS OF USE 1
COAGULATION AND METHODS OF USE 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match 99.8%; Score 616; DB 2; L. Best Local Similarity 100.0%; Pred. No. 2.9e-52; Matches 117; Conservative 0; Mismatches 0;
                                         Query Match 99.8%; Score 616; DB 1; I Best Local Similarity 100.0%; Pred. No. 2.9e-52; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTKI: U.C..
ZIP: 02109
COMPUTER REABLE FORM:
MEDLINH TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTEN: DOS
SOFTWARE: FASTEN: DOS
CURRENT APPLICATION NUMBER: US/09/293, 854
FILLING DATE: 16-Apr-1999
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION NUMBER: 08/814,806
FILING DATE: cluknown>
APPLICATION NUMBER: 08/814,806
FILING DATE: cluknown>
APPLICATION NUMBER: 08/814,806
FILING DATE: cluknown>
ATTORNEY/AGENT INFORMATION:
NAME: COTIGS9, PECEF REGISTRATION INFORMATION:
TELECOMMUNICATION DOS SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-293-854-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 117 amino acids
TYPE: amino acid
TYPE: anino acid
TYPE: anino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANIT. SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                           Sequence 4, Application US/09293854
Patent No. 6555319
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Wong, Hing C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jiao, Jin-an
                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-293-854-4
US-08-814-806-4
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1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60

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DD 1 EIGIGGGGFELWCGASAWOSCKTCSFTDNAWWGSIGGSLEADINDPWGGTILE 60

OQ 61 DOWFCGCATLTVAGSSTTAFMILSIDDSNAYFCARDTTALDFWGGTILT 60

61 DOWFCGCATLTVAGSSTTAFMILSIDSNAYFCARDTTALDFWGGTILTWSS 117

BESUL 3

US-667-468-139

US-667-468-130

US-667-468-130
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ADDRESSEE:
STREET: 15
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                                                                                                                                                                                                                               FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                              Matches
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Patent No. 6677436

GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: AADACH; HIDEKI
APPLICANT: YABUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY ACAINST HUMAN TISSUE PACTOR (TF) AND
TITLE OF INVENTION: HUMANIZED ANTIBODY ACAINST HUMANIZED ANTIBODY
TITLE OF INVENTION: HUMBER: US/09/647,468
CURRENT APPLICATION NUMBER: 053466/0289
CURRENT APPLICATION NUMBER: DCT/JP99/01768
PRIOR APPLICATION NUMBER: DCT/JP99/01768
PRIOR PLILING DATE: 1998-04-02
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE PATENTION VET. 2.1
SEQ ID NO 153
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (TF) AND
                                                                                                                                                                                                                             1 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60
                                                                                                                                                                                                1 BIOLOOSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
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                                                                                                                                                                                                                                                                                                  61 DONFKGKATLIVDKSSTTAFMHLNSLISDDSAVYFCAR-DVTTALDFWGQGTTLIVSS 117
                                                                                                                                                                                                                                                                                                                              61 DQNFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
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; OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF; OTHER INFORMATION: mouse monoclonal antibody ATR-3 US-09-647-468-140
                                                                                                                                                          1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10; Indels 1; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 154, Application US/09647468
Batent No. 6677436
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: ADACHI, HIDEKI
APPLICANT: ADACHI, HIDEKI
APPLICANT: YBUTA, NAOHIRO
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (1
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: PCT/JP99/01768
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence coding for H chain V region of ant-TF OTHER INFORMATION: mouse monoclonal antibody ATR-2
                                                                                                 Length 118;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 137;
                                                                                               84.5%; Score 521.5; DB 2; Length 83.9%; Pred. No. 3.9e-43; ive 8; Mismatches 10; Indels
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Best Local Similarity 83.9%; Pred. No. 4.6e-43;
Matches 99; Conservative 8; Mismatches 10
                                                                                            Query Match
Best Local Similarity 83.94
Matches 99; Conservative
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ORGANISM: Mus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 5
US-09-647-468-153
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US-09-647-468-154
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LENGTH: 137
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1 BIOLOOSGPELVKPGASVOVSCKTXGYSFTDYNVYWVROSHGKSLEWIGYIDPYNGITIY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 DONFKGKATLITVDKSSTIAFMHLNSLISDDSAVYFCAR-DVTTALDFWGQGTTLITVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         90 NQKFKGKATLIVDKSSSTAFMHLNSLTSEDSAVYYCARGGEGYYFDYWGQGTTLIVSS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
APPLICANT: Smith, Rodger
APPLICANT: Chiswell, David
APPLICANT: Chiswell, David
APPLICANT: Chiswell, Michael J.
APPLICANT: Fitzgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Fitzgerald, Kevin
APPLICANT: Martin, Mark T.
APPLICANT: Milliams, Richard C.
APPLICANT: Titmas, Richard C.
TITLE OF INVENTION: The Isolation and Production of
TITLE OF INVENTION: Catalytic Antibodies using Phage Technology
NUMBER OF SEQUENCES: 71
                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: Amino acid OTHER INFORMATION: sequence coding for H chain V region of ant-TF OTHER INFORMATION: mouse monoclonal antibody ATR-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1;
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COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/273,146
FLING DATE: 14-JUL-1994
CLASSIFICATION: 435
ATTONNEY/AGENT INFORMATION:
NAME: RYAN, JOHN W.
REGISTRATION NUMBER: 33,771
REBRENCE/DOCKET UNMBER: 33,771
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION: TELECOMMUNICATION:
                                                                                                                                                                                                                                                                                                                                                                                                   2;
                                                                                                                                                                                                                                                                                                                                                                                                Score 521.5; DB 2;
Pred. No. 4.6e-43;
8; Mismatches 10;
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[: 1530 East Jefferson St.
Rockville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; Sequence 55, Application US/08273146; Patent No. 5855885
PRIOR FILING DATE: 1995...
PRIOR APPLICATION NUMBER: JP 10-
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 154
LENGTH: 137
                                                                                                                                                                                                                                                                                                                                                                                                   84.5%;
83.9%;
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TYPE: amino acid
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    99; Conservative
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COMPUTER READABLE FORM:
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Best Local Similarity
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ORGANISM: Mus sp.
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TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 105:
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                      NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 158
LENGTH: 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: New York
STATE: New York
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  amino acid
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                                                                                                                          TYPE: PRT
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| Sequence 144, Application US/09647468
| Sequence 144, Application US/09647468
| Sequence 144, Application US/0964768
| Parent No. 6677436
| GENERAL INFORMATION:
| APPLICANT: SATO, KOH
| APPLICANT: ADACHI, HIDEKI
| APPLICANT: ADACHI, HUDEKI
| APPLICANT: ADACHI, HUDEKI
| PAPLICANT: ADACHI, HUDEKI
| PRIOR FILING DATE: 1099-04-02
| PRIOR FILING DATE: 1999-04-02
| PRIOR FILING DATE: 1999-04-03
| NUMBER OF SEQ ID NOS: 183
| SOFTWARE: Patentin Ver: 2.1
| LENGTH: 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF mouse OTHER INFORMATION: monoclonal antibody ATR-8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: SATO, KOH
APPLICANT: SATO, KOH
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
APPLICANT: ADACHI, HIDEKI
APPLICANT: ADACHI, HOMANIZED
ATITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REPERBANCE: 053466/029
CURRENT APPLICATION NUMBER: US/09/647,468
CURRENT FILING DATE: 1999-01768
PRIOR APPLICATION NUMBER: PCT/DP99/01768
PRIOR APPLICATION NUMBER: DCT/DP99/01768
PRIOR APPLICATION NUMBER: DCT/DP99/01768
                                                                                                                                                                        1 EIQLQOSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                    1. QVQLQQSGPELVKPGASVKVSCKASGYAFTNYNIYWVKQSHGKSLEWIGYIDPYSGGSSY 60
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                                                                                                                                                                                                                                                                      61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                               1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                          1; Gaps
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                                                                            Length 116;
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                                                                                                                       Indels
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                                                                       DB 1;
                                                                       Query Match 78.5%; Score 484.5; DB 1
Best Local Similarity 76.1%; Pred. No. 1.4e-39;
Matches 89; Conservative 15; Mismatches 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 158, Application US/09647468
Patent No. 6677436
GENERAL INFORMATION:
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nes 90; Conservative
MOLECULE TYPE: protein
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ORGANISM: Mus sp.
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          , MODECOLD ...
US-08-273-146-55
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Best Local S:
Matches 90
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20 DIQLQQSGPELVKPGASVKVSCKASGYSFTDYNIFWVKQSHGKSLEWIGYIDPYTGGTGY 79
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                                                                                                                                                                                                                                                                                       1 BIQLQOSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 NQKFNDKATLIYDKSSSTAFMHLNSLISEDSAVYYCARGFYYDYDCYWGQGTLVIVSA 137
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OTHER INFORMATION: Description of Artificial Sequence: Nucleotide OTHER INFORMATION: sequence coding for H chain V region of ant-TF OTHER INFORMATION: mouse monoclonal antibody ATR-8
                                                                                                                                                                                                                           ۲;
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                                                                                                                                                                 Length 137;
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                                                                                                                                                              Query Match
77.6%; Score 478.5; DB 2; Length 1
Best Local Similarity 76.3%; Pred. No. 6.5e-39;
Matches 90; Conservative 12; Mismatches 15; Indels
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Sequence 105, Application US/08672345C

Patent No. 59486F8

TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY

NUMBER OF SEQUENCES: 108

CORRESPONDENCE ADDRESS:

ADDRESSEE: Cooper and Dunham LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/672,345C
FILING DATE: 24-JUN-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERRANCE/DOCKET NUMBER: 0575/51400
TELECOMMUNICATION INFORMATION:
TELERHONE: 212-278 0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       15;
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Best Local Similarity 75.2%; Pred. No. 1.6e-38;
Matches 88; Conservative 13; Mismatches 15
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STREET: 1185 Avenue of the Americas
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Query Match
Best Local Similarity 75.2°
Matches 88; Conservative
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Best Local Similarity 74.64
Matches 88; Conservative
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ORGANISM: Mus Musculus
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ORGANISM: Mus sp.
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US-09-647-468-143
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                       JS-09-802-083-5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                     61 DONFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLIVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DONFKGKATLIVDKSSTTAFMILNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EIHLQQSGPELVKPGASVKLSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPHNGGIFY
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61 DONFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLIVSS
                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 116;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
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Sequence 90 Application US/09940727B

Patent No. 691391

GENERAL INCEMPATION:
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 0575/51400-B

CURRENT FILING DATE: 2002-09-04

PRIOR APPLICATION NUMBER: US/09/940,727B

CURRENT FILING DATE: 1998-12-28

PRIOR APPLICATION NUMBER: PCT/US97/10965

PRIOR APPLICATION NUMBER: 06/21,4,095

PRIOR FILING DATE: 1997-06-25

PRIOR FILING DATE: 1997-06-25

NUMBER OF SEQ ID NOS: 121

SEQ ID NO 90

TENNENT: 100 90
                                                                                                                         Sequence 90, Application US/09214095D
Patent No. 6280997
GENERAL INFORMATION:
APPLICANT: Landry, Donald
TITLE OF INVENTION: ANTI-COCAINE CATALYTIC ANTIBODY
FILE REFERENCE: 51400-4PCT-US
CURRENT APPLICATION NUMBER: US/09/214,095D
CURRENT FILING DATE: 1999-07-19
NUMBER OF SEQ ID NOS: 121
SOFTWARE: Patentin version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match 76.7%; Score 473.5; DB 2; Best Local Similarity 75.2%; Pred. No. 1.6e-38; Matches 88; Conservative 13; Mismatches 15;
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Best Local Similarity
Matches 88; Conserv
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                                                                                                       US-09-214-095D-90
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TYPE: PRT
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OTHER INFORMATION: Amino acid sequence of H chain V region of anti-TF mouse OTHER INFORMATION: monoclonal antibody ATR-7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 DIQLQQSGPELVKPGSSVKVSCKASGYSFPDYNIFWVKQSHGKSLEWIGYIDPYTGGTGY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 143, Application US/09647468

Sequence 143, Application US/09647468

Patent No. 6677436

GENERAL INFORMATION:
APPLICANT: SATO, KOH

APPLICANT: ADACH, HIDEKI

APPLICANT: YABUTA, NACHIRO

TITLE OF INVENTION: HUMANIZED ANTIBODY ACAINST HUMAN TISSUE FACTOR (TF) #

TITLE OF INVENTION: HUMBER: US/09/647,468

CURRENT PELING DATE: 1999-29

PRIOR PELING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: US/098-04

PRIOR PELING DATE: 1998-04-03

PRIOR FILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SEQ ID NO 143

LENGTH: 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
Sequence 5, Application US/09802083
; Patent No. 6703494
; GENERAL INFORMATION:
; APPLICANT: Kirchhofer, Daniel K.
; APPLICANT: Lowe, David G.
; APPLICANT: Lowe, David G.
; TITLE OF INVENTION: Anti-Tissue Factor Antibodies with Enhanced
; TITLE OF INVENTION: Anti-Cagulant Potency
; FILE REPERENCE: P1736R1
; CURRENT FILING DATE: 2001-03-08
; RIOR APPLICATION NUMBER: US/09/802,083
; CURRENT FILING DATE: 2000-03-16
; RIOR FILING DATE: 2000-03-16
; NUMBER OF SEQ ID NOS: 28
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 118;
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RESULT 15
US-09-647-468-157
Sequence 157, Application US/09647468
Sequence 157, Application US/09647468
Retent No. 6677436
GENERAL INFORMATION:
APPLICANT: SADO, KOH
TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMAN TISSUE FACTOR (TF) AND TITLE OF INVENTION: HUMANIZED ANTIBODY AGAINST HUMANIZED ANTIBODY
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
TITLE OF INVENTION: PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODY
FILE REFERENCE: 053466/0289
CURRENT FILING DATE: 2000-09-29
PRIOR APPLICATION NUMBER: UF(JP99)/01768
PRIOR FILING DATE: 1999-04-03
PRIOR PELING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PARENTIN Ver. 2.1
SEQ ID NO 157
LENGTH: 137
LENGTH: 137
LENGTH: 137
TYPE: RRT
ORGANISM: MUS SP.
FRATURE:
OTHER INFORMATION: mequence coding for H chain V region of ant-TF
US-09-647-468-157
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 76.1%; Score 469.5; DB 2; Length 137; Best Local Similarity 74.6%; Pred. No. 4.8e-38; Matches 88; Conservative 13; Mismatches 16; Indels 1; Gaps
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Search completed: April 18, 2006, 13:41:12 Job time : 48 secs

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GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd.
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OM protein - protein search, using sw model

April 18, 2006, 13:35:55 ; Search time 39 Seconds (without alignments) 288.650 Million cell updates/sec Run on:

US-10-764-140-4

1 EIQLQQSGPELVKPGASVQV......RDVTTALDFWGQGTTLTVSS 117 Perfect score: Sequence:

BLOSUM62 Scoring table:

Gapop 10.0 , Gapext 0.5

Searched:

283416 Total number of hits satisfying chosen parameters:

283416 segs, 96216763 residues

Minimum DB seq length: 0 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database

PIR_80:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		ko				
Result		Query				
o S	Score	Match	Length	8	ΔI	Description
1	468.5	75.9	137	7	25.	heavy chain p
7	465.5	~	139	~	A27609	heavy chain
e	463	75.	117	Н	MHMS4E	heavy chain
4	463	75.0	140	7	T01407	
S	461.5	74.	128	~	137267	heavy chain
9	460	7		-	MHMSJS	
7	452.5	73.3		7	F30502	heavy chain V
80	4	72.8	118	7	PL0200	nti-DNA autoanti
σ	448.5	72.7		7	809957	heavy chain
10	448	72.6	117	7	803305	heavy
11	446.5		120	~	A49982	heavy chain V
12	4	71.8	151	~	PL0011	heavy chain pr
13	ä		122	N	E37267	heavy chain
14	441.5	•	128	N	C37267	heavy
15	440		138	N	PH0105	i-digo
16	σ		135	~	PS0057	heavy chain
17	438.5		114	N	826319	heavy
	438	71.0	119	N	PH0099	heavy chain V
19	436		121	N	F37266	heavy chain V
20	ഗ	70.6	469	N	S37483	gamma-
21	433.5		118	-	MHMS38	Ig heavy chain V r
22	432		246	~	838950	Ig gamma chain - m
23	4.		446	N	S40295	Ig gamma-2a chain
24	o		122	~	PH0887	Id heavy chain V r
25	429.5	٠	128	N	A37267	neavy chain V
56	യ		. 113	~	855535	heavy
27	426		166	~	PL0012	neavy chain
28	425	68.9	121	~	H37266	eavi
29	423.5		108	~	PH0975	chain V

Ig heavy chain pre Ig heavy chain V-D	heavy		heavy	19 heavy chain V r Iq heavy chain V r Iq heavy chain Dre			Ig heavy chain V r anti-glycoprotein	
345249 309961	353285 240100	355528	5542 1584	PH1482 S04575	537 ISB1	534	5176	H0974
\$3	B53	PNG	SSE	S PH	See	S55	S25	PH
2 24	2 B53 2 PH0	2 PNC 2 SS5	2 855	2 PHI 2 SO	2 S66 1 HW	2 \$55	2 S	2 PH
0,0	00	01 00	~ -	140 2 PH1 140 2 SO	~ -	0	N N	~
138 2 8	119 2 1	150 2	116 2	0 0	131 2	113 2	117 2	113 2
68.4 138 2 8 68.2 117 2 8	119 2 1	68.2 150 2 68.0 113 2	67.9 116 2	140 2	67.8 131 2 67.7 136 1	67.7 113 2	67.7 117 2 67.7 120 2	67.6 113 2

ALIGNMENTS

RESULT 1
H32513
Ig heavy chain precursor V region (BXW16) - mouse
C;Species: Wus musculus (house mouse)
C;Date: 21-May-1990 #sequence_revision 31-Dec-1990 #text_change 21-Jan-2000
C;Lin: Invest: 82, 852-860, 1988
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Reference number: A94689; MUID:88331394; PMID:3138286
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: DNA
A;Molecule type: Inmunoglobulin V region; immunoglobulin homology
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;34-117/Domain: immunoglobulin homology < TWM>

Query Match 75.9%; Score 468.5; DB 2; Length 137; Best Local Similarity 75.4%; Pred. No. 1.3e-35; Matches 89; Conservative 14; Mismatches 14; Indels 1.

7; 1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60 20 BIQLQQSGAELVKPGASVKISCKASGYSFTGYNMAWVKQSHGKSLEWIGNINPYYGSTSY 79 Gaps 1; 셤 ઠે

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RESULT 2

A27609

Ig heavy chain precursor V region (I29) - mouse

C;Species: Mus musculus (house mouse)

C;Species: Mus musculus (house mouse)

C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999

C;Date: 15-Dec-1988 #sequence_revision 30-Jun-1991 #text_change 23-Jul-1999

R;Klein, D.; Nietupski, J.; Sirlin, S.; Stavnezer, J.

J. Immunol. 140, 1676-1684, 1988

A;Title: I.29 lymphoma cells express a nonmutated V-H gene before and after H chain swi
A;Reference number: A27609; MUID:88154467; PMID:3126234

A;Molecule type: DNA

A;Residues: 1-139 «KLB» A;Cross-references: UNIPARC:UP10000114D5D; EMBL:M19401; NID:g195441; PIDN:AAA38303.1; P

Aintrons: 16/1 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heteroctramer; immunoglobulin F;1-19/Domain: signal sequence #status predicted <SIG> F;20-139/Product: Ig heavy chain V region I29 #status predicted <VAR> F;34-117/Domain: immunoglobulin homology <IMM>

117 136

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Ig heavy chain V region (129) - mouse (Species: Mus musculus (house mouse) (Species: Mus musculus (house mouse) (Cjate: 18-Oct.1991 #sequence_revision 18-Oct.1991 #text_change 16-Aug-1996 (CjAccession: 137267 (CjAccessi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ig heavy chain V region (J558) - mouse (tentative sequence)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1991 #sequence_revision 30-Jun-1991 #text_change 09-Jul-2004
C;Accession: A26242
R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.
R;Schilling, J.; Clevinger, B.; Davie, J.M.; Hood, L.
A;Title: Amino acid sequence of homogeneous antibodies to dextran and DNA rearrangements!
A;Reference number: A26242; MUID:80078170; PMID:6765983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A,Cross-references: UNIPROT:P01757; UNIPARC:UPI00000270F2
A,Note: the sequences of 10 hybridoma proteins that also bind dextran differ from that s. C.Comment: This protein binds dextran.
C;Comment: This protein binds dextran.
C;Superfamily: immunoglobulin v region; immunoglobulin homology
C;Keywords: heterotetramer; hybridoma; immunoglobulin
F;15-98/Domain: immunoglobulin homology < IMM>
F;22-96/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DONFKGKATLIVDKSSTTAFWHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLIVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 IQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIYD
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               DONFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS
                                                     80 NQKFKGKATLIVDKSSSTAYMQLNSLISEDSAVYYCARDYDWYFDVWGAGTTVTVSS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: UNIPARC:UPI0000176C52
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterocetramer; immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
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71.5%; Pred. No. 5.1e-35;
tive 17; Mismatches 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Residues: 1-128 <RUF>
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Matches
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Cipate: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
Cipate: 30-Nov-1979 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
Cipate: X0Chemistry 21, St15-5424, 1982
Biochemistry 21, St15-5424, 1982
A; Title: Complete amino acid sequence of a mouse mu chain: homology among heavy chain characterance number: A02039; MUID:83075344; PMID:6816276
A; Accession: A02039
A; Molecule type: protein
A; Research A02039
A; Molecule type: protein
A; Residues: L17 < KEH>
A; Cross-references: UNIPROT:P01756; UNIPARC:UP100000270F1
C; Comment: This protein binds dextran.
C; Superfamily: immunoglobulin V region; immunoglobulin homology
C; Keywords: glycoprotein; heterotetramer; immunoglobulin
C; Superfamily: immunoglobulin homology < IMM>
F; 15-99/Domain: immunoglobulin homology < IMM>
F; 15-99/Domain: immunoglobulin homology < IMM>
F; 15-96/Disulfide bonds: #status predicted
F; 15-96/Disulfide bonds: #status predicted
F; 15-96/Disulfide bonds: #status predicted
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[G.Species Mus sp. (mouse)

[G.Species Mus sp. (mouse)

[G.Date: 20-8p-1999 #sequence_revision 20-Sep-1999 #text_change 20-Jun-2000

[G.Accession: T01407

[G.Accession: T01407

M.Trakahashi, S.; Matsuura, Y.; Taniguchi, T.; Tamura, H.; Bitoh, S.; Onishi, S.; Yamamot Mirobiol. Immunol. 36, 855-863, 1992.

M.Trile: Molecular analysis of immunoglobulin heavy chain genes coding for idiotypic and A; Reference number: Z14317; MUD: 93116638; PMID: 1474935

A; Reference number: Z14317; MUD: 93116638; PMID: 1474935

A; Residues: translated from GB/EMBL/DDBJ

A; Residues: Lanslated Arom GB/EMBL/DDBJ

A; Residues: Lanslated Arom GB/EMBL/DDBJ

A; Residues: Lanslated Arom GB/EMBL/DDBJ

A; Residues: Inmunoglobulin V region; immunoglobulin homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            i heavy chain V region (MOPC 104E) - mouse (tentative sequence)
Species: Mus musculus (house mouse)
Date: 30-Nov-1999 #sequence_revision 14-Nov-1983 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BIQLQOSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
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               Length 139;
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               DB 2;
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       75.4%; Score 465.5; DB 2
72.5%; Pred. No. 2.4e-35;
ive 18; Mismatches 12
Query Match
Best Local Similarity 72.5%
Matches 87; Conservative
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Best Local Similarity 74.48
Matches 87; Conservative
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C;Species: Mus musculus (house mouse)
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 23-Jul-1999
C;Date: 12-Feb-19957
R;Reininger, L.; Shibata, T.; Ozaki, S.; Shirai, T.; Jaton, J.C.; Izui, S.
Eur. J. Immunol. 20, 771-777, 1990
Bur. J. Immunol. 20, 771-777, 1990
A;Title: Variable region sequences of pathogenic anti-mouse red blood cell autoantibodi
A;Reference number: $09955; MUID:90269328; PMID:2347362
                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: UNIPARC:UPI0000115E5C; EMBL:X51845; NID:955244; PIDN:CAA36138.1; PI C;Superfemally: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin homology <1MM>
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C;Date: 30-Sep-1991 #sequence revision 30-Sep-1991 #text_change 23-Jul-1999
C;Accession: J.10044; S05276; S03305
R;Van Gave, V.H.; Naeve, C.W.; Metzger, D.W.
J. Exp. Med. 167, 1841-1848, 1988
A;Title: Do antibodies recognize amino acid side chains of protein antigens independent A;Reference number: JL0043; MUID:882S8372; PMID:2455014
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A;Residues: 1-116,'T' <MET>
A;Cross-references: UNIPARC:UPI0000115DB3; EMBL:X12381; NID:g52094; PIDN:CAA30939.1; PI
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C;Species: Mus musculus (house mouse)
C;Date: 10-Nov-1995 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
C;Accession: A49982
R;Lin, C.; Kieber-Emmons, T.; Villalobos, A.P.; Foster, M.H.; Wahlgren, C.; Kleyman, T..
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1 EIOLOOSGPELVKPGASVOVSCKTXGYSFTDYNVYWVROSHGKSLEWIGYIDPYNGITIY 60
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R;Merzger, D.W.
submitted to the EMBL Data Library, July 1988
A;Reference number: S05276
A;Accession: S05276
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(1)
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;; Pred. No. 6.7e-34;
14; Mismatches 13
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Best Local Similarity 72.6%;
Matches 85; Conservative 1
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Best Local Similarity 72.00,
Conservative 1
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A; Residues: 1-112 <REI>
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A; Residues: 1-117 <VAN>
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R; Smith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A; Mith, R.G.; Voss Jr., E.W.
Mol. Immunol. 27, 463-470, 1990
A; Title: Variable region primary structures of monoclonal anti-DNA autoantibodies from N A; Reference number: PLO198; MUID:90309768; PMID:2114528
A; Accession: PLO200
A; Molecule type: mRNA
A; Residues: 1-118 <SMI>A; Residues: 1-118 <SMI>A; Residues: UNIPARC:UPI0000113784; GB:X53641; NID:g50193; PIDN:CAA37692.1; PID:g5.Superfamily: immunoglobulin homology of MM>F; 15-99/Domain: immunoglobulin homology of MM>F; 15-99/Domain: immunoglobulin homology of MM>F; 15-96/DkRegion: complementarity-determining 2
F; 99-110/Region: complementarity-determining 3
F; 99-110/Region: complementarity-determining 3
F; 99-1106/Region: Jr region
F; 107-118/Region: Jr region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
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           NQKFKGKATLTVDKSSSTAYMQLNSLTSEDSAVYYCARDRYWYFDVWGAGTTVTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                anti-DNA autoantibody BV16-19, heavy chain V region - mouse (fragment) C; Species: Mus musculus (house mouse) C; Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
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S09957
Ig heavy chain V-D-J region (106-10E) - mouse (fragment)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               73.3%; Score 452.5; DB 2, 73.1%; Pred. No. 3.1e-34; ive 12; Mismatches 17,
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72.0%; Pred. No. 6.3e-34;
cive 14; Mismatches 15
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Best Local Similarity 72.0°
Matches 85; Conservative
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Ig heavy chain V region (Py69) - mouse
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Best Local Similarity
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Best Local Similarity
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Accession: E37267
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Cipate: 30-Unn-1992 #teat_change 21-Jan-2000
Cipate: 30-Unn-1992 #teatuence_revision 30-Jun-1992 #text_change 21-Jan-2000
Cipate: 30-Unn-1992 #teatuence_revision 30-Jun-1992 #text_change 21-Jan-2000
Cipate: 30-Unn-1992 #teatuence_revision 30-Jun-1992 #text_change 21-Jan-2000
Cipate: 31-40, 1988
A;Title: Structural basis of stimulatory anti-idiotypic antibodies.
A;Recession: PL0011; MUD: 88142863; PMID: 3125424
A;Accession: PL0011; MUD: 88142863; PMID: 3125424
A;Accession: PL0011
A;Molecule type: mRNA
A;Recences: UNPARC:UPI0000176D36
A;Experimental source: cell line 4C11
C;Comment: This protein is an anti-idiotypic antibody that induces an anti-phosphorylcha
C;Superfamily: immunoglobulin V region; immunoglobulin Negion 4C11 #status predicted <MAT>
F;0-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F;0-136/Product: Ig heavy chain V region 4C11 #status predicted <MAT>
F;0-136/Product: Ig heavy chain V region 4C11 #status predicted <CRP>
F;0-136/Product: Complementarity-determining 2
F;69-55/Region: complementarity-determining 3
F;118-125/Region: Complementarity-determining 2
F;118-125/Region: Complementarity-determining 3
F;118-125/Region: Complementarity-determining 3
F;118-125/Region: Complementarity-determining 3
                                                                                                                                                                                                   NID:9452096; PIDN:AAA98740.1; PID
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61 NQNFKDTASLTVDKSSTSAYMELHSLTSEDSAVYXCARFNYYGHYT--MDYWGQGTSVTV 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain precursor V region (4C11) - mouse (fragment)
C;Species: Mus musculus (house mouse)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ig heavy chain V region (Py42) - mouse
C;Species: Mus musculus (house mouse)
C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_change 21-Jan-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
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            A;Title: Topology of an amiloride-binding protein.
A;Reference number: A49982; MUID:94132051; PMID:8300613
A;Reference number: A49982; MUID:94132051; PMID:8300613
A;Retue: preliminary
A;Rolecule type: mRNA
A;Residues: 1-120 <LIN>
A;Cross-references: UNIPARC:UPIO000114AA4; GB:L24802; NID:945209
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterocetramer; immunoglobulin
P;15-98/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                          13;
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Best Local Similarity 68.9%; Pred. No. 1.1e-33;
Matches 84; Conservative 18; Mismatches 13
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R;Ruff-Jamison, S.; Campos-Gonzalez, R.; Glenney Jr., J.R.
J. Biol. Chem. 266, 6607-6613, 1991
A;Fitle: Heavy and light chain variable region sequences and antibody properties of anti
A;Reference number: A38740; MUID:91177923; PMID:1706720
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C;Species: Mus musculus (house mouse)
C;Accession: PH0105
R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, M.; Hudson, N.W.; Margolies, M.N.; Seldman, J.G. R;Near, R.I.; Ng, S.C.; Mudgett-Hunter, C.; Hudson, N.W.; Margolies, M.N.; Seldman, J.G. A;Title: Heavy and light chain contributions to antigen binding in an anti-digoxin chain A;Reference number: PH0105; MUID:91015092; PMID:2120577
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                                                                                                                                                                                A; Status: preliminary; not compared with conceptual translation
                                                                                                                                                                                                                                                                                                              C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary; not compared with conceptual translation A;Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: UNIPARC:UP10000176B3A
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer: immunoglobulin
F;19-102/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            11; Indels
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C;Date: 18-Oct-1991 #sequence_revision 18-Oct-1991 #text_chan;
C;Accession: C37267
Accession: C37267
J. Biol. Chem. 266, 6607-6613, 1991
A;Title: Heavy and light chain variable region sequences and A;Reference number: A38740; MUID:91177923; PMID:176720
A;Reference number: A38740; MUID:91177923; PMID:176720
                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 2;
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66.7%; Pred. No. 3.3e-33;
ive 19; Mismatches 15
                                                                                                                                                                                                                                                                                                                                                                              F;19-102/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                           A;Molecule type: mRNA
A;Residues: 1-122 <RUF>
A;Cross-references: UNIPARC:UPI0000176B3C
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A;Accession: PH0105
A;Status: preliminary
A;Molecule type: mRNA
A;Molecule type: mRNA
A;Residues: 1-138 <NRA>
A;Cross-references: UNIPARC:UPI0000115EC4; GB:X56622; GB:S44836; NID:g49875; PIDN:CAA399
C;Superfamily: immunoglobulin V region; immunoglobulin homology
F;34-117/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                     2; Gaps
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Sequence 4 Application US/09990586

| Dublication No. US20030109680A1
| GENERAL INFORMATION:
| APPLICANT: JIAO, JIN-AN
| APPLICANT: JIAO, JIN-AN
| TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
| TITLE OF INVENTION: OF USE THEREOF
| TITLE OF UNIVENTION: OF USE THEREOF
| TITLE OF USE THEREOF
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| TITLE OF U
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Sequence 4, Application US/20030176664A1
Publication No US20030176664A1
GENERAL INFORMATION:
APPLICANT: JINO, JIN-AN
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: MOSQUERA, LUIS A.
TITLE OF INVENTION: USE OF ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING TITLE OF INVENTION: THROMBOSES
TITLE OF INVENTION: USE OF ANTI-TISSUE CURRENT APPLICATION NUMBER: US/10/310,113
CURRENT APPLICATION NUMBER: 09/990,586
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US-10-165-732A-5
US-10-745-455-5
US-10-745-625-143
US-10-462-062-157
US-10-488-074-67
US-10-488-074-71
US-10-389-155-15
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US-10-389-155-15
US-10-389-155-15
US-10-389-417-60
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US-09-990-586-4
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296.279 Million cell updates/sec
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1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
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6: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-10-210-113-4

US-10-290-417-4

US-10-290-417-4

US-10-764-140-4

US-10-764-140-4

US-10-764-140-4

US-10-462-062-139

US-10-462-062-153

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US-10-77-2

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US-10-27-80-2

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US-10-462-062-158
US-10-488-074-69
US-09-940-7278-90
US-09-802-083-5
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US-10-500-696-2
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FUDLication No. US20030190705A1
GENERAL INFORMATION:
APPLICANT: APPLICANT: APPLICANT: STINSON, JEFFREY L.
APPLICANT: MOSQUERA, LUIS A.
TITLE OF INVENTION METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE OF INVENTION METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
CURRENT FILING DATE: 2002-12-23
FRIOR PAPLICATION NUMBER: 09/990,586
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/343,306
PRIOR PLILING DATE: 2001-10-29
PRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 174
SOFTWARE PECENTIN VUMBER: 05/293,854
NUMBER OF SEQ ID NOS: 174
SOFTWARE PECENTIN VOR: 2.1
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                                                                                                                                                                                                                                                                                                                 100.0%; Score 617; DB 4; Length 117; 99.1%; Pred. No. 4.7e-52;
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PRIOR APPLICATION NUMBER: 60/343,306
PRIOR FILING DATE: 2001-10-29
PRIOR PLING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
PRIOR PILING DATE: 1997-03-10
PRIOR FILING DATE: 1997-03-10
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PALENTIN VET. 2.1
SEQ ID NO 4
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Best Local Similarity 99.1<sup>3</sup>
Matches 116; Conservative
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ORGANISM: Homo sapiens
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ORGANISM: Murine ap.
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% Sequence 4, Application US/09293854; Sequence 4, Application US/09293854; Patent No. US20020168357A1; GENERAL INFORMATION:

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1 EIGLQOSGPELVKPGASVQVSCK(XXXSTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EYSFIDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
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Esperanza, Nieves
Esperanza, Luepschen
Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Esperanza, Nieves
Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                             NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 99.8%; Score 616; DB 3; Best Local Similarity 100.0%; Pred. No. 5.9e-52; Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                        COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COMPATIBLE
COMPATING SYSTEM: DOS
SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-APr-1999
CLASSIFICATION: <UNKNOWN>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/814,806
FILING DATE: «Unknown»
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-4400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-293-854-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 4, Application US/10293417; Publication No. US20030082636A1
GENERAL INFORMATION: APPLICANT: Wong, Hing C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 EIQLQOSGPELVKPGASVQVSCK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 117 amino acids TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-10-293-417-4
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1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            61 DQNFKGKATLIYDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLIYSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  61 DONFKGKATLIVDKSSTIAFMHLNSLISDDSAVYFCARDVITALDFWGQGTILIVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match

99.8%; Score 616; DB 5; Length 117;
Best Local Similarity 100.0%; Pred. No. 5.9e-52;
Matches 117; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM COMPATIBLE
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FRACECY Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/618,338
FILING DATE: 11-Uul-2003
CLASSIFICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
APPLICATION NUMBER: 08/814,806
FILING DATE: 16-Apr-1999
ATTORNEY/ACENT INFORMATION:
NAME: COFLOSS, PETER F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUTCATION INFORMATION:
                                                                                                                                                                                               ; OTHER INFORMATION: Variable amino acid US-10-764-140-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 117 amino acids TYPE: amino acid
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TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 4:
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         NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIn Ver. 3.2
                                                                                              TYPE: PRT
ORGANISM: Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                NAME/KEY: MOD RES
LOCATION: (25)
                                                                             LENGTH: 117
                                 SOFTWARE: E
                                                                                                                                               FEATURE:
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Sequence 4, Application US/10764140

Publication No. US20040229282A1

GENERAL INFORMATION:

APPLICANT: WONG, HING C.

APPLICANT: WONG, HING C.

APPLICANT: WONG, JIN-AN

TITLE OF INVENTION: OF USE THEREOF

FILE REFERENCE: 59918 (71758)

CURRENT APPLICATION NUMBER: 10/291,417

PRIOR APPLICATION NUMBER: 10/293,417

PRIOR APPLICATION NUMBER: 09/293,854

PRIOR FILING DATE: 2002-04-16

PRIOR FILING DATE: 2002-04-16

PRIOR FILING DATE: 2002-04-16

PRIOR FILING DATE: 2002-04-16

PRIOR APPLICATION NUMBER: 08/814,806

PRIOR FILING DATE: 2002-03-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 DONFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
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ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
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                                                                                                                                                                         COMPUTER: IEM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/293,417
FILING DATE: 12-No. US20030082636A1-2002
CLASSIFICATION: CURROWN>
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99.8%; Score 616; DB 4; I
Best Local Similarity 100.0%; Pred. No. 5.9e-52;
Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
APPLICATION NUMBER: 08/814,806
FILING DATE: <unknown>
ATTORNEY/AGENT INFORMATION:
NAME: COT1689, Peter F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FRAGMENT TYPE: N-terminal
CRIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-10-293-417-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-533-6440
TELERA: cUnknown>
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 117 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                 ZIP: 02109 COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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US-10-462-062-140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 139, Application US/10462062

Publication No. US20040044187A1

GENERAL INFORMATION:

APPLICANT: ADACHI, HIDEKI

TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMANIZED ANTIBODIES

FILE REFERENCE: 053466-0360

CURRENT APPLICATION NUMBER: US/10/462,062

CURRENT PILING DATE: 2003-06-16

PRIOR PILING DATE: 1999-04-02

PRIOR APPLICATION NUMBER: DT/JP99/01768

PRIOR PILING DATE: 1998-04-02

PRIOR PILING DATE: 1998-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE: PALENTIN VET: 2.1

SEQ ID NO 139

LENGTH: 118
                                                                                                                                                                                                                 ö
                                                                                                                                                                                                                                                                                   1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
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Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT FILING NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR APPLICATION NUMBER: PCT/JP99/01768
                                                                                                                                                                                                                                                           1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        61 DONFKGKATLITVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLITVSS 117
                                                                                                                                                                                                                                                                                                                                                     61 DONFKGKATLITVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                               61 DQNFKGKATLIVDKSSTTAFMHINSLISDDSAVYFCARDVITALDFWGQCTTLIVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 BIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY
                                                                                                                                                                                                               0; Сарв
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1; Gaps
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                                                                                                                                                                Length 117;
                                                                                                                                                                                                            Indels
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                                                                                                                                                              Query Match
99.8%; Score 616; DB 5;
Best Local Similarity 100.0%; Pred. No. 5.9e-52;
Matches 117; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        84.5%; Score 521.5; DB 4, 83.9%; Pred. No. 8.6e-43; iive 8; Mismatches 10,
                                                            ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO:
US-10-618-338-4
                     ANTI-SENSE: NO
FRAGMENT TYPE: N-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity 83.9°
Matches 99, Conservative
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  RESULT 8
US-10-462-062-139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-10-462-062-140
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OTHER INFORMATION: Description of Artificial Sequence: Amino acid sequence of OTHER INFORMATION: H chain V region of anti TF mouse monoclonal antibody ATR-3
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Sequence 153, Application US/10462062

Publication No. US20040044187A1

Sequence 153, Application US/10462062

Publication No. US20040044187A1

APPLICANT: AAPACH, HIDEXI

TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)

TITLE OF INVENTION: HUMANIZED ANTIBODIES OF PRODUCTION OF THE HUMANIZED ANTIBODIES

FILE REFERENCE: 053466-0360

CURRENT FILING DATE: 2003-06-16

PRIOR APPLICATION NUMBER: US/10/462,062

CURRENT FILING DATE: 1999-04-02

PRIOR FILING DATE: 1999-04-03

NUMBER OF SEQ ID NOS: 183

SOFTWARE: PATENTING US: 2.1

SEQ ID NO 153

LENGTH: 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EIQLQOSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 EIQLQQSGPELVKPGASVKVSCKASGYSFTDYNMYWVKQSHGKSLEWIGYIDPYNGGTIY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DONFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DONFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTALDFWGQGTTLTVSS 117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
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Pred. No. 1e-42;
8; Mismatches 10; Indels 1:
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION WINBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PATENTIN Ver. 2.1
SEQ ID NO 140
LENGTH: 118
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US-10-462-062-154
IS-10-462-062-154
; Sequence 154, Application US/10462062
; Publication No. US20040044187A1
; GENERAL INFORMATION:
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83.9%;
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ORGANISM: Artificial Sequence
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Best Local Similarity 83.94
Matches 99; Conservative
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Best Local Similarity
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61 DONFKGKATLIVDKSSTTAFMILNSLISDDSAVYFCAR---DVTTALDFWGQGTTLIVSS 117
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                                          Sequence 2, Application US/10505747

Sequence 2, Application US/10505747

Sublication No. US20050106145A1

GENERAL INFORMATION:

APPLICANT: DE SANTIS, RITA

APPLICANT: ANASTASI, ANNA MARIA

TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY

FILE REPERBNES: 2018-141

CURRENT APPLICATION NUMBER: US/10/505,747

CURRENT FILING DATE: 2004-08-25

FRIOR PELLING DATE: 2002-02-66

NUMBER OF SEQ ID NOS: 22

SOFTWARE: PATENTIN Ver. 2.1

SEQ ID NO.2

LENGTH: 120

TYPE: PRT
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Publication No. US2003015251A1

GENERAL INNORMATION:
APPLICANT: JOHAK, ZDENKA

APPLICANT: JOHAK, ZDENKA

APPLICANT: TAYLOR, ALEXANDER

TITLE OF INVENTION: ANIT-ALPHABETA3 HUMANIZED MONOCLONAL

FILE REFERENCE: P50629C1

CURRENT APPLICATION NUMBER: US/10/223,880

CURRENT APPLICATION NUMBER: 09/380,910

PRIOR APPLICATION NUMBER: 09/380,910

PRIOR PILING DATE: 1999-09-10

PRIOR FILING DATE: 1999-03-12

PRIOR FILING DATE: 1999-03-12

NUMBER OF SEQ ID NOS: 45

SEQ ID NOS: 45

SEQ ID NOS: 45

SEQ ID NOS: 45
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4.9e-40;
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Best Local Similarity
Matches 89; Conserv
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                   APPLICANT: ADACHI, HIDBKI
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 2003-06-16
PRIOR FILING DATE: 1999-04-02
PRIOR FILING DATE: 1999-04-03
PRIOR FILING DATE: 1999-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver: 2.1
SEQ ID NO 154
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
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Fublication No. US20040005643A1
GENERAL INFORMATION:
TITLE OF INVENTION: ANTI-HUMAN TENASCIN MONOCLONAL ANTIBODY
FILE REFERENCE: 2818-141
CURRENT APPLICATION NUMBER: US/10/372,719
CURRENT APPLICATION NUMBER: 60/359,299
FRIOR FILING DATE: 2002-02-26
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin Ver. 2.1
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82.9%; Score 511.5; DB 4;
Best Local Similarity 76.7%; Pred. No. 8.2e-42;
Matches 92; Conservative 17; Mismatches 8;
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ORGANISM: Artificial Sequence
APPLICANT: SATO, KOH
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LENGTH: 120
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RESULT 15

US-10-774-076-2

US-10-774-076-2

Sequence 2, Application US/10774076

Publication No. US20040210040A1

GENERAL INFORMATION:
APPLICANT: Landolfi, et al.,
TITLE OF INVENTION: Amphiregulin Antibodies and Their Use to Treat Cancer and
TITLE OF INVENTION: Psoriasis
FILE REPERENCE: 05882.0064-NPUS01

CURRENT APPLICATION NUMBER: US/10/774,076

CURRENT FILING DATE: 2004-02-06

NUMBER OF SEQ ID NOS: 39

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 119

TYPE: PRT

ORGANISM: mus sp.
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Search completed: April 18, 2006, 13:44:03 Job time : 166 secs

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A76486B1 Mus muscu
A78220107 Sequence
A7820108 Sequence
A7859279 Sequence
A7869279 Sequence
A78745 Sequence
A7876746 Sequence
A7878142 Sequence
A7878143 Sequence
A7878143 Sequence
A7803540 Sequence
              M36761 Mouse Ig re
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172603 Sequence 4
A225594 Mus muscu
AX591700 Mus muscu
AC120404 Mus muscu
M36757 Mouse Ig re
BD222154 Immunolog
AX006748 Sequence
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M57988 Mouse IgK c
M36756 Mouse Ig re
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AR220109 Sequence
AR369281 Sequence
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Unclassified.
1 (bases Lto 321)
Wong,H.C., Jiao,J.-A., Nieves,E.Liliana. and Luepschen,L.
Antibodies for inhibiting blood coagulation and methods of use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GGGAAATCTCCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGGTCCCATCA
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100.0%; Score 321; DB 6;
Best Local Similarity 100.0%; Pred. No. 8.8e-88;
Matches 321; Conservative 0; Mismatches 0;
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/mol_type="unassigned DNA"
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Location/Qualifiers
1. .321
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Sequence 1 from patent US 5986065.
AR087417
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AR369279
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AR46980
AR476745
AR478142
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XXU34924
MUSIGKAAAK
MUSIGKAAAK
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MMU235949
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AC120404
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AR220107
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ACCESSION
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KEYWORDS
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ORGANISM
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TITLE
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FEATURES
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AR087417
 ORIGIN
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AR50760 Mouse Ig re
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AR302092 Synthetic
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E10064 Synthetic D
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Sato,K., Adachi,H. and Yabuta,N. Humanized antibody against human tissue factor (TF) and process of production of the humanized antibody Patent: US 6677436-A 12 13-JAN-2004; Chugai Seiyaku Kabushiki Kaisha, Tokyo; JPX;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAAACCA 120
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                                                                            Unknown.
Unclassified.
I (bases 1 to 321)
Wong, H.C., Jiao, J.-A., Nieves, E.L. and Luepschen, L.
Antibodies for inhibiting blood coagulation and methods of use thereof
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                                                                                                                                                                          Patent: US 6555319-A 1 29-APR-2003;
Sunol Molecular Corporation; Miramar, FL
Location/Qualifiers
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Sequence 12 from patent US 6677436.
AR455626.
AR452626.1 GI:42684507
Sequence 1 from patent US 6555319.

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10-MAR-1998 JP 1998539703
HING C WONG, JIN AN JIAO, ESPERANZA LILIANA NIEVES, LAWRENCE
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synthetic construct
other sequences, artificial sequences.
1 (bases 1 to 321)
Wong,H.C., Jiao,J.A., Nieves,E.L. and Luepschen,L.
Antibodies for inhibiting blood coagulation and methods of use
sunot MOLECULAR CORP.
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Matches 321; Conservative 0; Mismatches 0;

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    ^organism="synthetic construct"
/mol_type="genomic DNA"
/db_xref="taxon:32630"

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ROD 14-APR-2000
anti-viral
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/product="variable region of immunoglobulin kappa chain"
/portein id="CAA74341"
/db_xref="G1:2222726"
/tranalation="nogMTGSPASQSASLGESVTITCLASQTIGTWLAWYQQKPCKSP
QLLIYAATSLADGVPSRFSGSGGTKFSFKISSLQAEDFVSYYCQQLYSTPYTFGGGT
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Cupit, P.M.

Direct Submission

Submitted (24-JUN-1997) Cupit P.M., Molecular and Cell Biology,

University of Aberdeen, Institute of Medical Science, Foresterhill,

Aberdeen, AB15 2ZD SCOTLAND, UK
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1 (bases 1 to 318)

Lorenzen, N., Olesen, N.J. and Jorgensen, P.E.

Weutralization of E Egreed virus pathogenicity to cell cultures and fish by monoclonal antibodies to the viral G protein

J. Gen. Virol. 71 (Pt 3), 561-567 (1990)
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                                                                                                                                                                                                                                            immunoglobulin; kappa chain; light chain; variable region.
Mus musculus (house mouse)
Mus musculus
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Pred. No. 1.2e-78;
0; Mismatches 16;
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/product="variable region
/evidence=experimental
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/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
                                                         355 GGGACCAAGCTGGAAATAAAA 375
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/codon_start=1
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                                                                                                                                                                                     GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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                                                                                                                                                                                                                                                                                                235 AGGTTCAGTGGTAGTGGATCTGGCACAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 294
                                                                                                                                                                                                                                                                                                                                     GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Sato, ", Adachi, H. and Yabuta, N.
Humanized antibody against human tissue factor (TF) and
production of the humanized antibody
Patent: US 6677435-A 13 13-JAN-2004;
Chugai Seiyaku Kabushiki Kaisha; Tokyo;
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Pred. No. 2.2e-79;
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AR452627
AR452627.1 GI:42684508
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/mol_type="genomic DNA"
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/note="Ig kappa-chain V-J-region"
Codon gtart=1
/protein id="AAA38757.1"
/db_xref="G1:196620"
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/organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:10090"
                                         321
                                                          301 GGCACCAAGCTGGAAATCAAA 321
                                          301 GGGACCAAGCTGGAGCTGAAA
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                                                                       241 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTACACGTTCGGAGGG 300
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                                                        GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                                                                                                                                                                                                                          X90900.1 GI:1518326
antibody light chain; variable region.
Mus musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Musinae; Mus.
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                181 AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGGCGCTACAGGCT
AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTTTTTCAAGATCAGCAGCCTACAGGCT
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Submitted (17-AUG-1995) M. Geiser, CIBA-GEIGY LTD, CDDT,
K-681.5.46, CH-4002, Basel, SWITZERLAND
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
/producl="antlbody light chain variable region"
/protein_id="CAA62408.1"
|b_xref="G1:1518327"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db xref="taxon:10090"
/cell_type="lymphocytes"
/tissue_type="spleen"
/dev stage="12 weeks old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /mol_type="genomic DNA"
/strain="BALB/c"
                                                                                                                                                                                                                                                                                                                                                                                Geiser, M. and Kretzschmar, T.
Unpublished
                                                                                                                                        301 GGGACCAAGCTCGAGAT 317
                                                                                                               301 GGGACCAAGCTGGAGCT 317
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Best Local Similarity 94.1
Matches 302; Conservative
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Geiser, M.
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181
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AUTHORS
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MUSIGKADP 124 bp mRNA linear ROD 27-APR-1993
Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds.
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Qlliyaatsladgvpsrfsgsgsgtkfsfkixxlqaedfvsyycqqlystpwtfgggt
Xlbikr"
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                                       241 GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCGTGGACGTTCGGTGGA 300
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Draft entry and computer-readable sequence for (J. Immunol. (1990) In press) kindly submitted by S.H.Clarke, 18-JUL-1990.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 324)
Clarke, S., Rickert, R., Wloch, M.K., Staudt, L., Gerhard, W. and Weigert, W. Wloch, M.K., Staudt, L., Gerhard, W. and Weigert, M. Weigert, M. With Shils, Gecondary response to the Sb site of influenza virus hemagglutinin. Nonrandom silent mutation and unequal numbers of wind Vk mutations
J. Immunol. 145 (7), 2286-2296 (1990)
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J-region; V-region; immunoglobulin light chain; processed gene.
Mus musculus (house mouse)
Mus musculus
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PAT 10-APR-2001
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/mol type="unassigned DNA"

/db_xref="taxon:32610"

/db xref="taxon:32630"

/note="bescription of Artificial Sequence:single chain

antibody gene (BUI) inserted into E. coli pCDNA3 plasmid

(Invitorgen)"
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synthetic construct
synthetic construct
construct
leaduences; artificial sequences.

(bases 1 to 1135)
Lorenzen,N., Cupit,P.M., Einer-Jensen,K., Lorenzen,E., Ahrens,P.,
Secombes,C.J. and Cunningham,C.
Immunoprophylaxis in fish by injection of mouse antibody genes
Nat. Biotechnol. 18 (11), 1177-1180 (2000)
                                                                                                                                                                                                                         Secombes, C.J., Cunningham, C. and Lorenzen, N.
Monoclonal antibody 3flh10 neutralising vhsv (viral haemorrhagic
espticaemia virub,
Patent: WO 0121800-A 1 29-WAR-2001;
ABERDEEN UNIVERSITY (GB); Statens Veterinaere Serumlaboratorium
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Synthetic construct single chain antibody BUI gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity 93.5%; Score 287.4; DB 6; Length Similarity 93.5%; Pred. No. 1.9e-77; D0; Conservative 0; Mismatches 21; Indels
                                                            linear
                                                            DNA
                                                                                                                                                                                        other sequences; artificial sequences.
                                                          AX100597 1135 bp Sequence 1 from Patent WO0121800.
                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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AF302092.1 GI:11692742
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synthetic construct
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Best Local Simil
Matches 300; C
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ACCESSION
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KEYWORDS
SOURCE
                                                                         DEFINITION
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VERSION
KEYWORDS
SOURCE
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TITLE
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AUTHORS
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                                                                                                                              MUSIGKADN 324 bp mRNA linear ROD 27-APR-1993
MOUSE IG rearranged kappa-chain mRNA V-J region, partial cds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon start=1
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/db xref="G1:196616"
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QLLIYAATSLADGVPSRRSGSGSTKFSFKIXXLQAEDFVSYYCQQLYSTPWTFGGGT
RLEIKR"
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Draft entry and computer-readable sequence for [J. Immunol. (1990) In press] kindly submited by S.H.Clarke, 18-JUL-1990.
Location/Qualifiers
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                                                                                                                                                                                                                                                               Euteleostomi;
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The BALB/c secondary response to the Sb site of influenza virus hemsgalutinin. Nonrandom silent mutation and unequal numbers of and Vk mutations
J. Immunol. 145 (7), 2286-2296 (1990)
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                                                                                                                                                                                                   J-region; V-region; immunoglobulin light chain; processed gene Mus musculus (house mouse)
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Clarke, S., Rickert, R., Wloch, M.K., Staudt, L., Gerhard, W.
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Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Eute
Mammalia, Butheria, Buarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 324;
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Pred. No. 7.8e-78;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1. .324
/organism="Mus musculus"
/mol_type="mRNA"
/db_xref="taxon:10090"
GGGACCAAGCTGGAGCTGAAA 321
                   GGGACCAAGCTGGAGCTGAAA 321
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Best Local Similarity 93.1%;
Matches 299; Conservative
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                                                                                     RESULT 9
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-1. ->324
/note="19" kappa-chain V-J-region"
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/db_xref="GI:196618"
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QLLIYAATSLADGVPSRFSGSGGGTKFSFKIXXLQAEDFVSYYCQQLYSTPWTFGGGT
RLEIKR"
                              The BALB/C secondary response to the Sb site of influenza virus hemagglutinin. Nonrandom silent mutation and unequal numbers of VH and Vk mutations.

Journal of William (1), 2286-2296 (1990)

Journal of (1990)

Journal 
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Synthetic DNA fragments.

CON Synthetic DNA fragments.

Synthetic DNA fragments.

CON 120055.1 GI:22026691

Synthetic GI:22026691

Synthetified

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LABABE 1 to 1228)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 287.2; DB 9;
Pred. No. 2.4e-77;
0; Mismatches 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Mus musculus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    301 GGGACCAAGCTGGAGCTGAAA 321
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Matches 298; Conservative
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VTGYSITSGYYWTWIRQFPGNKLEWMGYISYDGTNNYNPSLTNRISITRDTSKNQFFL
KLKSVTTEDTATYYCVRGIYYGNDWPAYWGQGTTVTVSSEGKSSGSGSESKVDDIELT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      QSPASQSASLGESVTITCLASQTIGTWLAWYQQKPGKSPQLLIYAATSLADGVPSRFS
GSGSGTKFSFKISSLQAEDFVSYYCQQLYSTPYTFGGGTKLEIKRTVAAPSVFIFPPS
DEQLKSGTASVVCLLNNFYPREAKVQWKVDNALQSGNSQESVTEQDSKDSTYSLSSTL
2 (bases 1 to 1135)
Ahrens, P. and Cupit, P.
Direct Submission
Submitted (01-SEP-2000) Fish Section, Danish Veterinary Laboratory,
Hangovej 2, Aarhus DK-8200, Denmark
Location/Qualifiers
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Mouse Ig rearranged kappa-chain mRNA V-J region, partial cds.
M36759
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Clarke, S., Rickert, R., Wloch, M.K., Staudt, L., Gerhard, W. and
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llarity 93.5%; Pred. No. 1.9e-77;
Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                            1. .1135
/organism="synthetic construct"
/mol_type="genomic DNA"
mol_xref="taxon:32630"
1. .9
/note="derived from Invitrogen pCDNA3"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TLSKADYEKHKVYACEVTHQGLSSPVTKSFNRGES"
1126. 1135
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/db_xref="GI:11692743"
                                                                                                                                                                                                                                                                                                                                                                                                            13. .1122
/note="Mus musculus antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GGGACCAAGCTCGAGATCAAA 798
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PI KATOU IKUNOSHIN
PC CIZNIS/09//A61K39/145, CO7K16/10, CIZNI/21, CIZPZ1/08, GOIN33/53,
PC GOIN33/569,
PC GOIN33/569,
PC GOIN33/569,
CG GOIN33/577, (CIZNIS/09, CIZRI:19), (CIZPZ1/08, PC CIZRI:19);
CG Strandedness: Single;
CC strandedness: Single;
FH Key Location/Qualifiers
FH FF Source 1. .1300
FT Masc_feature 1. .1300
FT Masc_feature 1. .1300
FT /note='DNA encoding a fused protein'.
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PN JP 1995265077-A/23
PD 17-C07-1995
PF 30-MAR-1994 JP 1994082693
PI OKNOY YOSHINOBU, OSHIMA ATSUSHI, YOSHIOKA HIROFUMI, PI
TAKAHATA TAKASHI,
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                                          Length 1228;
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                                     Query Match

89.4%; Score 287; DB 6;
Best Local Similarity 93.7%; Pred. No. 2.5e-77;
Matches 299; Conservative 0; Mismatches 20;
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Okuno, Y., Oshima, A., Yoshioka, H., Takaha
Ma CODING FOR ANTIBODY VARIABLE REGION
PATENE: JP 1995265077-A 23 17-OCT-1995;
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/organism="unidentified"
/mol_type="genomic DNA"
/db_xref="taxon:32644"
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Synthetic DNA fragments.
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PD 17-OCT-1995
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PF 30-MAR-1994 UP 1994082693
PF 30-MAR-1994 UP 1994082693
PF 30-MAR-1994 UP 1994082693
PI TAKAHATA TAKASHI,
PI KATOU IKUNOSHIN
PC C12N15/09/A61K39/145,C07K16/10,C12N1/21,C12P21/08,G01N33/53,PC G01N33/577,(C12N15/09,C12R1:91),(C12N1/21,C12R1:19),(C12P21/08,PC C12R1:19);
CC 8trandedness: Single;
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Unknown.
Unclassified.
1 (bases 1 to 1228)
1 (bases 1 to 1228)
1 (bases 2 to 1228)
2 (buno, Y., Oshima, A., Yoshioka, H., Takabatake, T. and Kato, I.
DNA coding for variable region to human influenza A type virus
Patent: US 5684146-A 35 04-NOV-1997;
Location/Qualifiers
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Pred. No. 2.5e-77;
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Sequence 35 from patent US 5684146.
172625 173625.1 GI:3008764

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Best Local Similarity 93.7%;
Matches 299; Conservative (
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Query Match

89.4%; Score 287; DB 6; Length 1300;
Best Local Similarity 93.7%; Pred. No. 2.5e-77;
Matches 299; Conservative 0; Mismatches 20; Indels
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Search completed: April 18, 2006, 19:05:23 Job time : 2419 secs

Anti-huma

Aa288324 Anti-zeta
Aad7166 Single ch
Aad21540 Single ch
Aad21540 Single ch
Ab633655 Anti-T-ce
Ab833654 Anti-T-ce
Ad488101 Wild type
Ad708284 DNA encod
AAX7211 BCFV-KA16
AAX87210 Wild-type
AAX87210 Wild-type
AAX97155 Single ch
AA23165 Anti-T-ce
Ad48103 Single ch
AA23165 Anti-T-ce
Ad48103 Single ch
Ab653656 Anti-T-ce
Ad488103 Single ch
Ab653656 Anti-T-ce
Ad75599 Brythrocy
AA27599 Brythrocy
AA27599 Brythrocy
AA25599 Brythrocy
AA989511 HEV relat

Aat35973 Anti-huma

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Title: Perfect score:

Sequence:

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OM nucleic

Run on:

Scoring table:

Searched:

Database

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Human; anti-tissue factor light chain variable region; H36.D2.B7; anti-tissue factor heavy chain variable region; inhibition; antibody; blood coagulation; thrombosis; restenosis; thromboembolic condition; cardiovascular; infection; neoplastic disease; clot; diagnosis; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human anti-tissue factor light chain variable region encoding cDNA.
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/product= "anti-tissue factor light chain variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        region"
/note= "no stop codon given"
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AAD27166
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AAD21541
AAD21540
ABS53654
ABS53654
AD788101
AD789102
ADR03284
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AAX87210
AAX870423
AAD21542
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AD68103
AD83285
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AAX95434
AAB99634
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P-PSDB; AAW71287.
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 Ad135002 Murine an
Adw06807 Murine H3
Adw06807 Murine H3
Adw07325 Mouse ant
Adx10336 H36.D2.B7
Adx33012 Anti-tiss
Adx33013 Anti-tiss
Adx113 High-func
Aar04179 C179FV-PP
Adx1605 High-func
Aar04180 ScFV-PP
Adx51609 High-func
Adx51611 High-func
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                                                                                        April 18, 2006, 18:23:59; Search time 456 Seconds (without alignments) 4691.593 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Description
                                                                                                                                                                                 1 gacattcagatgacccagtc......ggaccaagctggagctgaaa
         5.1.7
Biocceleration Ltd.
                                                                                                                                                                                                                                                                                     9993994
                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                      4996997 segs, 3332346308 residues
          GenCore version
Copyright (c).1993 - 2006
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Maximum Match 1008
Listing first 45 summaries
                                                                nucleic search, using sw model
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ADU006807
ADW07325
ADZ40336
ACC58568
AAZ33012
AAZ33013
AAZ31613
AAF76338
AAF76338
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New antibody to human tissue factor - used for, e.g. treating thrombosis or restenosis or thromboembolic conditions associated with cardiovascular, infectious or neoplastic disease.

Score

Result

Mosquera LA;

Stinson JR,

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06-AUG-2003; 2003WO-US024637.
                                                                                                                        29-AUG-2002; 2002US-00230880
                                                                                                                                                           (SUNO-) SUNOL MOLECULAR CORP.
                    WO2004020579-A2.
                                                   11-MAR-2004
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                                             The present sequence encodes the human anti-tissue factor light chain variable region from an antibody that binds native human tissue factor (TF) and does not bind non-native TF. The antibody capable of specifically binding native TF may be used for inhibiting blood capulation and also for reducing TF levels in a mammal. The antibodies coagulation and also for reducing TF levels in a mammal. The antibodies can be used, e.g. to treat thromboses, particularly to prevent or inhibit restenosis, or other thromboses following an invasive medical procedure cuch as arterial or cardiac surgery (e.g. angioplasty, endarterectomy, deployment of a stent, use of catheter, graft implantation or use of an arteriovenous shunt). The antibodies can also be used as a carrier for drugs, particularly pharmaceuticals targered for interaction with a blood clot such as streptokinase, itssue phasminogen activator (t-PA) or urokinase, or a cytotoxic agent by conjugating a suitable toxin to the antibodies can be used for treating a trimbody. Further the antibodies can be used for treating a trimbody condition associated with cardiovascular disease, an coplastic disease or as a thrombolytic agent. The antibodies can also be used for detection and diagnosis
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                                                                                                                                                                                                                                                                                                                                                                                                                                         Indels
                                                                                                                                                                                                                                                                                                                                                                     Seguence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                     100.0%; Score 321; DB 2;
100.0%; Pred. No. 1.1e-92;
ative 0; Mismatches 0;
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                Claim 11; Fig 1A; 53pp; English.
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Best Local Similarity
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This invention relates to a novel method for producing a humanised antibody variable (V) domain or its fragment by optimising sequence similarity between individual antibody framework regions (FRs) in order to identify suitable human FRs (huFRs). Specifically, it refers in order immune system molecules i.e. humanised monoclonal antibodies that exhibit suitable binding affinity with reduced immunospenicity in humans. The present invention describes a method of mutagenising DNA of non-human FRs to encode humanised FRs having an amino acid sequence that is substantially identical to the selected human FR previously identified through sequence similarity searching. As such, this method provides through sequence similarity searching. As such, this method provides humanised light or heavy chain V domains of the sequence huFRI-CDRI-huFR2-CDR2-huFR3-CDR3-huFR4, which can be used as therapeutic or diagnostic products to treat and/ or diagnose diseases in humans and animals.

Furthermore, the method expands the number of best fit possibilities that can be generated and provides a rational basis for assembling nearly all humanised immune system molecules of interest. This polynucleotide sequence is a murine anti-tissue factor light chain antibody H36-D2-B7
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                                                                                                                                    Producing humanized antibodies for diagnostic and therapeutic purposes comprises optimizing similarity between individual antibody framework regions to help identify human framework regions suitable for making the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       100.0%; Score 321; DB 12;
100.0%; Pred. No. 1.1e-92;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 1; 137pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches 321; Conservative
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WPI; 2004-239169/22.
P-PSDB; ADL35003.
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AGGTTCAGTGGCAGTGGCATCTGGCACAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT

181 181

GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT

GGGACCAAGCTGGAGCTGAAA 321

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Key

ADU06807

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GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCCATTCACGTTCGGGGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Blood-clotting; light chain variable region; inflammation; antiinflammatcory; antibody; 88; ti8sue factor; sepsis; disseminated intravascular coagulation; anticoagulant; hematological disease; thrombosis; lung injury; respiratory-gen.; respiratory distress syndrome; Immunosuppressive; Antibacterial; Antianthritic; Antianemic; anemia; rheumacoid arthritis; glomerulomephritis; multiple sclerosis; psoriasis; sjogren's syndrome; inflammatory bowel disease.
                                                                                                                                                                                                                                                                 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA
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        Length 321;
                                           Indela
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/note= "No start or stop codon shown"
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    100.0%; Score 321; DB 13; 100.0%; Pred. No. 1.1e-92;
                                             ö
                                           0; Mismatches
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/product= "Light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGGACCAAGCTGGAGCTGAAA 321
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22-JAN-2004; 2004US-0538892P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ADW07325 standard; cDNA; 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-JUN-2004; 2004WO-US017900
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Query Match
Best Local Similarity 100.
Matches 321, Conservative
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P-PSDB; ADW07326.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel method for treating or preventing (MI) septic shock syndrome in a mammal, involving administering to the mammal an effective amount of an antibody that binds native human tissue factor and does not substantially bind non-native tissue factor, where the factor X binding to the complex is inhibited and the administration is sufficient to prevent or treat the septic shock syndrome in the mammal. In (MI), the antibody has the binding specificity for native human tissue factor about equal to or greater than H36.D2.B7 (ATC HB-12255), and is a monoclonal chimeric antibody. An antibody of the invention has mathadererial and immunosuppressive activity, and acts as an inhibitor of binding between factor X or factor Via and tissue factor/factor VIIa complex. The present sequence encodes the light chain variable region of the murine antibody of the invention, H36.D2.B7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Treating or preventing septic shock syndrome in mammal, involves administering antibody that binds native human tissue factor and does not substantially bind non-native tissue factor.
                                                                                                                                                                                                                                                                                                                                       "Antibody H36.D2.B7 light chain variable
                                                                                                                                                                            ds; gene; septic shock syndrome; tissue factor; antibacterial; immunosuppressive; antibody; antibody therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= b
70. .90
/*tag= c
/note= "Encodes hypervariable region CDR1"
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'note= "Encodes hypervariable region CDR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   roce= "Encodes hypervariable region CDR3"
                                                                                                                                   Murine H36.D2.B7 antibody VL encoding DNA SEQ ID NO:1.
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                                                                                                                                                                                                                                                                                                                                                                                              ^hote= "No start/stop codon given"
/transl_except= (pos:16. .21, aa:Ser)
16. .21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 43; SEQ ID NO 1; 28pp; English
                                                                                                                                                                                                                                                               Location/Qualifiers
1. .321
                  ADU06807 standard; DNA; 321 BP
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16-APR-1999; 99US-00293854.
12-NOV-2002; 2002US-00293417.
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/product=
                                                                                                (first entry)
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P-PSDB; ADU06808.
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                                                                                                                                                                                                                                        Mus musculus
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                                                                                                10-FEB-2005
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                                                         ADU06807;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Wong HC,
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Preventing or treating sepsis or inflammation in mammals comprises administering a humanized or chimeric antibody that binds to a human tissue factor to form a complex in which factor X or IX binding to the complex is inhibited. region of the anti-TF antibody (wild-type). Disclosure; SEQ ID NO 1; 109pp; English.

Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;

Claim 11; SEQ ID NO 1; 36pp; English

ö 240 300 61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120 300 61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180 9 9 GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAGTGTCACC AGGTTCAGTGGCAGTGGATCTGGCACAAATTTTTTTCAAGATCAGCAGCCTACAGGCT 181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT Gaps ö Length 321; Indels Query Match 100.0%; Score 321; DB 14; Best Local Similarity 100.0%; Pred. No. 1.1e-92; Matches 321; Conservative 0; Mismatches 0; GGGACCAAGCTGGAGCTGAAA 321 121 181 241 301 g ઠ 유 8 δ ద ò 셤 ઠે 셤 δ g

H36.D2.B7 anti-tissue factor light chain variable region encoding DNA. (first entry) 14-JUL-2005 **8**84888

ADZ40936 standard; DNA; 321

ADZ40936

ADZ40936;

Antibodies binding to native human tissue factor without substantial binding to non-native tissue factor, useful for inhibiting blood coagulation, for reducing tissue factor levels in a mammal, and for 1. .321
/*tag= a
/*tod= "H36.D2.B7 anti-tissue factor light chain
variable region" antibody, tissue factor, blood-clotting, anticoagulant, vasotropic, thrombolytic, cardiovascular disease, infectious disease, neoplasm; thrombosis, restenosis, light chain variable region, gene; ds. Location/Qualifiers 10-MAR-1997; 97US-00814806. 16-APR-1999; 99US-00293854. 12-NOV-2002; 2002US-00293417. 11-JUL-2003; 2003US-00618338 (SUNO-) SUNOL MOLECULAR CORP Wen J; detecting tissue factor. WPI; 2005-344279/35. P-PSDB; ADZ40937. Wong HC, US2005089929-A1. Homo sapiens 28-APR-2005. Synthetic. Jiao J, Key

The invention relates to an antibody (I) that binds native human tissue factor and does not substantially bind non-native tissue factor. Also clescribed: (I) an isolated nucleic acid (II) comprising a sequence encoding at least a portion of an antibody that binds native human tissue factor; (2) a recombinant vector (IV) comprising (II), where (IV) can express at least a portion of an antibody that binds native human tissue complexes with native tissue factor and factor X binding (MI) blood complexes with native tissue factor and factor X binding to the complex complexes with native tissue factor and factor X binding to the complex is inhibited; (S) reducing (M2) tissue factor levels in a mammal by administering the antibody covalently linked to a cell toxin or to an effector molecule to provide complement—fixing ability and antibody.

CC defector molecule to provide complement—fixing ability and antibody cordinated cytotoxicity, where the antibody contacts cells expressing tissue factor to reduce tissue factor levels in the mammal; contacting the sample with the antibody (I), where the antibody is and (6) detecting the sample with the antibody (I), where the antibody is and contacting the sample with the antibody (I), where the antibody is contacting tissue factor in a biological sample. (I) is useful for inhibiting blood coagulation in a mammal complexed at thromboembolic condition associated with the treatment of a thromboembolic condition associated with conversion contents and testenosis. The antibodies of the invention content as thrombosis and restenosis. The antibodies of the invention content as thrombosis and restenosis. The antibodies of the invention of especially bind to non-native or denatured tissue factor and do not substantially bind to non-native or denatured tissue factor. The antibodies prevent conversion of factor X to its activated form factor. The interpretation of the tester sequence encodes the H36.D2.B7 anti-tissue factor light chain variable region.

Sequence 321 BP; 85 A; 80 C; 73 G; 83 T; 0 U; 0 Other;

Gaps ö 100.0%; Score 321; DB 14; Length 321; 100.0%; Pred. No. 1.1e-92; trive 0; Mismatches 0; Indels 0; Best Local Similarity 100. Matches 321; Conservative Query Match

us-10-764-140-1.rng

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The present sequence is the coding sequence for the light chain variable region (VL) of anti-recombinant human tissue factor (TF) murine antibody H36.D2.B7 (ATCC HB-12255). The invention relates to antibodies, especially humanized H36.D2.B7, that provide superior anticoagulant activity by binding native human TF with high affinity and specificity. The antibodies bind human TF, either alone or present in a TF.Factor VIIa complex, effectively preventing Factor X (or Factor IX) binding to TF or the complex, and thereby reducing blood coagulation. The humanized antibodies are useful for inhibiting blood coagulation or blood clot formation, anglogenesis, tumour metastases or inflammation in a mammal. They are also useful as drug carriers, as cycotoxic agents, for reducing TF levels in mammals, and for in vivo diagnosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             241 GAAGATTTGTAAATTA-TTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGC 299
241 GAAGATTTTGTAAATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGC 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody;
ATR-2; ATR-3; ATR-4; ATR-5; ATR-7; ATR-8; thrombotic disease; DIC;
disseminated intravascular coagulation; immunogenicity; chimeric; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Anti-tissue factor mouse monoclonal antibody ATR-2 L chain V region DNA
                                                                                                                                                                                                                                                                                                                                                                                                    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTGGGAGAAAGTGTCACC
                                                                                                                                                                                                                                                                                                                                                                           1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
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                                                                                                                                                                                                                                                                                            Score 310; DB 9; Length 322;
Pred. No. 3.8e-89;
0; Mismatches 0; Indels
                                                                                                                                                                                                                                                          Sequence 322 BP; 85 A; 80 C; 73 G; 84 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGGGACCAAGCTGGAGCTGAAA 321
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                                                                                                                                                                                                                                                                                                                Best Local Similarity 59., Matches 321; Conservative
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/tag= a
/partial
/product= "H36.D2.B7 VL"
/transl_except= (pos:256. .259,aa:Tyr)
/note= "this codon has an apparent 1 nucleotide insertion
which alters the reading frame; the CDS has no start or
stop codon"
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                      GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTCTGGGAGAAGTGTCACC
                                                                           ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA
                                                                                                                                                      GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGGTCCCATCA
                                                                                                                                                                                                                                 181 AGGTTCAGTGGCAGTGGATCTGGCACAAATTTTTCTTTCAAGATCAGCAGCCTACAGGCT
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antiinflammatory; mouse; gene; 88.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Anti-tissue factor antibody H36.D2.B7 VL coding sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ACC58568 standard; cDNA; 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-OCT-2001; 2001US-0343306P.
21-NOV-2001; 2001US-00990586.
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P-PSDB; ABR42699.
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99WO-JP001768 98JP-00091850

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Humanised antibody recognizing human tissue factor, used for treatment of
                                                                                                                                                                                                                                          disseminated intravascular coagulation.
                                                                                                                     (CHUS ) CHUGAI SEIYAKU KK.
                                                                                                                                                                                WPI; 1999-620204/53
                                                                                                                                                  Adachi H,
                                                                                                                                                                                               P-PSDB; AAY52762
                                                           02-APR-1999;
                                                                                        03-APR-1998;
 WO9951743-A1
                             14-OCT-1999.
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                                                                                                                                                  Sato K,
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                                                                                                              The present invention describes chimeric antibody (Ab) heavy (H) chains containing the variable region of the H chain of a mouse monoclonal Ab chain of a human Ab. The variable region is one of six specified the H chain of a human Ab. The variable region is one of six specified sequences (which are the H chain variable regions from mouse monoclonal Ab's ATR-2,3,4,5,7 or 8). Also described are chimeric Ab light (L) chains containing the variable region of the L chain of a mouse monoclonal Ab recognising human tissue factor (hTF) and the constant region of the L chain of a human Ab, the variable region being one of six specified sequences (which are the L chain variable regions from mouse monoclonal Ab recognising human tissue factor (hTF) and the constant for the treatment and prevention of thrombotic disease, especially of disseminated intravascular coagulation (DIC). The humanised antibody has the high hTF binding activity of the mouse monoclonal antibody but greatly reduced immunogenalcity. AAA233001 to AAA23301 and Y527007 to AAA25767 represent
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGAAATCTCCTCAGGTCCTGATTTATGCTGCAACCAGCTTGGCAGATGGGGGTCCCATCA 234
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human tissue factor; TF; humanised; antibody; mouse monoclonal antibody; ATR-2; ATR-3; ATR-4; ATR-7; ATR-8; thrombotic disease; DIC; disseminated intravascular coagulation; immunogenicity; chimeric; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Anti-tissue factor mouse monoclonal antibody ATR-3 L chain V region DNA.
                                          Humanised antibody recognizing human tissue factor, used for treatment
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0
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Pred. No. 6.5e-84;
0; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                              Sequence 375 BP; 96 A; 89 C; 92 G; 98 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                       DB 2;
                                                                                        Example 1; Page 190-191; 291pp; Japanese
                                                           disseminated intravascular coagulation.
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                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 91.54;
Best Local Similarity 94.74;
Matches 304; Conservative
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WPI; 1999-620204/53
              P-PSDB; AAY52761
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The present invention describes chimeric antibody (Ab) heavy (H) chains containing the variable region of the H chain of a mouse monoclonal Ab crecognising human tassue factor (hTF) and the constant region of the H chain of a human Ab. The variable region is one of six specified sequences (which are the H chain variable regions from mouse monoclonal Ab TRR-2.3,4.5,7 or 8). Also described are chimeric Ab light (L) chains containing the variable region of the L chain of a mouse monoclonal Ab recognising human tissue factor (hTF) and the constant region of the L chain of a human Ab, the variable region being one of six specified sequences (which are the L chain variable regions from mouse monoclonal C chain of a human Ab, the variable region being one of six specified sequences (which are the L chain variable regions from mouse monoclonal c not prevention of thrombotic disease, especially of disseminated intravascular coagulation (DIC). The humanised antibody has the high hTF binding activity of the mouse monoclonal antibody but greatly reduced immunogenicity. AA233001 to AA233001 and Y527007 represent invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       91.0%; Score 292.2; DB 2; Length 375; 94.4%; Pred. No. 2.1e-83; Indels 0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 375 BP; 96 A; 88 C; 93 G; 98 T; 0 U; 0 Other;
Example 1; Page 192; 291pp; Japanese.
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Matches 303; Conservative
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The invention relates to a non-infectious nucleic acid construct encoding are recombinant (e.g., single chain) antibody molecule. The nucleic acid construct is adapted for in vivo establishment of protective immunity to an infectious disease in an animal, or is formulated for in vivo prevention of an allergic reaction to an allergen or a reaction caused by the presence of a toxic substance in an animal. Constructs of the invention are thus useful for treating infectious disease caused by viral haemorrhagic septicaemia virus (VHSV) (fish), infectious haemotopoietic fish), bovine viral diarrhoea virus, pseudorables virus (pigg), plasmocytosis virus (mink), feline leuksemia virus, human immunodeficiency virus, and hepatitis A virus (human). Genetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New non-infectious nucleic acid construct encoding recombinant antibody molecule, useful for conferring protective immunity to infectious diseases, preventing allergic reactions or reactions caused by toxins in
                                                                                                                                                                                                                                                                             Anti-VHSV; single chain antibody BUI; ScAb; scFv; monoclonal antibody 3F1H10; variable region; antiviral; anti-allergy; human kappa light chain constant domain; vaccine; gene therapy; rainbow trout TGF-bera signal peptide; transforming growth factor beta; genetic prophylaxis; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         *tag= a
'note= "Derived from Invitrogen pCDNA3"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= c
/product= "Single chain antibody BUl"
                                                                                                                                                                                                                                    Anti-VHSV single chain antibody BU1-encoding DNA.
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(STAT-) STATENS VETERINAERE SERUMLABORATOTIUM.
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/note= "BU1 insert region"
1126. .1135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
852 GGTACCAAGCTGGAAATCAAA 872
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                                                                                                       AAF76338 standard; DNA; 1135
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Mus musculus.
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misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Synthetic.
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                                                                                     AAF7633(
ID AA)
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                                                                                                                             The invention relates to a method of selecting a high-functioning protein which comprises constructing a protein-coding DNA library, transcribing DNAs, attaching a spacer to the 3' end of transcribed RNAs and constructing a library of molecules assigned to genotype and phenotype in a cell-free translation system, treating the library of assigned amplecules, binding an assigned molecule to a target molecule and amplifying nucleic and The method is useful for selecting a high-functioning protein by selecting a protein interacting with a target molecule. The method is useful for manufacturing a protein which interacts with a target useful for manufacturing a protein which interacts with a target suspense and hypertension. The method is rapid and useful for treating cancer and hypertension. The method is rapid and efficient. The present sequence represents a high-functioning protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selecting a high-functioning protein which is useful for treating cancer and hypertension, comprises selecting a protein interacting with a target
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0; Gaps
                                                                                                    cytostatic; hypotensive; nucleic acid library; cancer; neoplasm;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 90.0%; Score 289; DB 14; Length 949; Best Local Similarity 93.8%; Pred. No. 3.3e-82; Matches 301; Conservative 0; Mismatches 20; Indels (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 949 BP; 248 A; 220 C; 259 G; 222 T; 0 U; 0 Other;
                                                        High-functioning protein related DNA SEQ ID NO 114
                                                                                                                      hypertension; cardiovascular disease; ds; gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 114; 92pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGACCAAGCTGGAGCTGAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                               Kojoh K;
                                                                                                                                                                                                                                                                                            15-OCT-2004; 2004WO-JP015290.
                                                                                                                                                                                                                                                                                                                                         15-OCT-2003; 2003JP-00355702
               30-JUN-2005 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                            Tabata N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2005-346216/35.
                                                                                                                                                                                                                                                                                                                                                                                  (UYKE-) UNIV KEIO.
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                                                                                                                                                                                                         WO2005035751-A1
                                                                                                                                                                 Unidentified
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                                                                                                                                                                                                                                                  21-APR-2005
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This sequence encodes the C179Fv-PP fusion polypeptide. The encoded sequence is an anti-human influenza A type virus antibody. The antibody recognises the stem region of the hemagglutinin (HA) molecule of the HIM1 and H2N2 subtypes of human influenza A type virus, and shows neutralisation activity against these two subtypes. The antibody shows no recognition of the H3N2 subtype. Artificial antibodies (such as this) and polypeptides are useful in the diagnosis and treatment of human influenza. As the antibodies recognise the stem region of the HA molecule changes. This provides an advantage over current vaccines, as the virus periodically alters it's HA molecule
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               589 GACATCGAGCTCACCCAGTCTCCTGCCTCCCAGTCTGCCATCTCGGGAGAAAGTGTCACC 648
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gene encoding variable region of anti-human influenza A type virus antibody - useful for prodn. of artificial antibodies.
                                                             "variable light chain-Fc fusion protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                         Ikunoshin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 1300;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1300 BP; 393 A; 319 C; 289 G; 299 T; 0 U; 0 Other;
                                                                                                                                                  /*tag= e horbing domain-like structure"
1102 - 1275
/*tag= f
                                                                                                                                                                                                                         /note= "Fc binding domain-like structure"
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         "variable heavy chain region"
                                                                                                                                                                                                                                                                                                                                                                                                                                       Takashi T,
                                                                                                                 "variable light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 287; DB 2;
Pred. No. 1.7e-81;
0; Mismatches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                       Atsushi O, Hirofumi Y,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 4; Page 32-35; 42pp; English.
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                                            /*tag= b
/product= '
601. .902
                                                                                                /*tag= d
/product= '
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                                                                                                                                  928. .1101
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Best Local Similarity 93.7
Matches 299; Conservative
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                                                                                                                                                                                                                                                                                                                                                                    30-MAR-1994;
                                                                                 misc_feature
                                                                                                                                  misc_feature
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prophylaxis methods using such constructs are useful for the transient protection of individuals against exposure to pathogens or toxins where con efficient vaccines are available, for inducing the synthesis of antibodies of a desired specificity for use in immunocompromised cantibodies of a desired specificity for use in immunocompromised cantibodies. And for protecting an individual against an allergic administration of plasmid-borne genes do not involve specific activation of the immune system in the individual. Prophylaxis against infectious diseases takes place without any side effects such as the transfer of infectious diseases or induction of hypersensitivity following repeated administration. The single chain antibodies will be systemically distributed by the body fluids and protect the individual if infection with the pathogen occurs. The present sequence represents a portion of a construct of the invention which encodes a single chain antibody. Bull is derived from the variable regions of the VHSV-reactive murine monoclonal antibody from the variable regions of the YHSV-reactive murine monoclonal antibody beta (TGF-beta) signal peptide at the N- terminus (to ensure secretion of the single chain antibody) and the human kappa light chain constant constant (used as a tag to facilitate detection) at the C-terminus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GAAGAITITIGIAAAITAITACIGICAACAAGITITACAGITICICCAITCGGIGCI 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      118 GAAGATTTTGTAAGTTATTACTGTCAACTTTACAGTACTCCGTACACGTTCGGAGGG 777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis;
haemagglutinin; variable heavy chain; therapy; ds.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              478 GACATCGAGCTCACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match

89.5%; Score 287.4; DB 4; Length 1135;
Best Local Similarity 93.5%; Pred. No. 1.2e-81;
Matches 300; Conservative 0; Mismatches 21; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1135 BP; 298 A; 293 C; 273 G; 271 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Variable heavy chain region"
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//roduct= "Variable h
/product= c
/*teg= c
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                                                                                                      851
                                                                                                                                                                                                                                                                                                                                                                                                                          Antibody; human; influenza type A virus; H1N1; H2N2; H3N2; HA; diagnosis; haemagglutinin; variable heavy chain; therapy; ds.
     GAAGATTTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTGGACGTTCGGTGGA
                                                                 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gene encoding variable region of anti-human influenza A type virus antibody - useful for prodn. of artificial antibodies.
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/note= "Fc binding domain-like structure"
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1030. .1203
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product= "variable light chain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "variable heavy chain"
                                                                                                                                                                                                                                                                          AAT04180 standard; cDNA to mRNA; 1228 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 4; Page 36-38; 42pp; English.
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                                                                                                                                        GGGACCAAGCTGGAGCTGAAA 321
                                                                                                                                                                           872
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                                                                                                                                                                         GGCACCAAGCTGGAAATCAAA
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529. .830
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Selecting a high-functioning protein which is useful for treating cancer and hypertension, comprises selecting a protein interacting with a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          552 GACATICAGAIGACACAGITICCIGCCICCCAGITIGCAICITIGGAGAGAAGIGICAIC 611
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   612 Arcacardecridecaagreagacearregracarderrageargeraregaaacea 671
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGAAATCTCCTCAGCTCCTGATTTATGCTGCAACCAGCTGGGCAGATGGGGGTCCCATCA 731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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                                                                                                                                                                                                                                                                  cytostatic; hypotensive; nucleic acid library; cancer; neoplasm; hypertension; cardiovascular disease; ds; gene.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                              High-functioning protein related DNA SEQ ID NO 106.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 285.8; DB 14;
Pred. No. 3.6e-81;
0; Mismatches 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; SEQ ID NO 106; 92pp; Japanese.
Kojoh K;
                                                                                                                  BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                          15-OCT-2004; 2004WO-JP015290.
                                                                                                              ADZ51605 standard; DNA; 949
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               15-OCT-2003; 2003JP-00355702
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         cch 89.0%;
al Similarity 93.1%;
299; Conservative
                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Tabata N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2005-346216/35.
P-PSDB; ADZ51606.
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Best Local Similarity
Matches 299; Conserv
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                                                                                                                                                                                                                                                                                                                                                                 WO2005035751-A1.
                                                                                                                                                                                                                                                                                                                         Unidentified
                                                                                                                                                                                         30-JUN-2005
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      related DNA
                                                                                                                                                     ADZ51605;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            molecule.
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The invention relates to a changeable region of mouse monoclonal antibody recognising surface antigen preSI epitope of hepatitis B virus and gene. This polynucleotide sequence relates to a 324nt DNA of the invention
                                                                                                                                                                                                                            ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
                                                                                                                                                                                                                                                                                   121 GGGAAATCTCCCTCAGCTCCTGATTTATGCTGCAACCAGCTTGGCAGATGGGGTCCCCATCA 180
                                                                                                                                                                                                                                                                                                                                                                                             Selecting a high-functioning protein which is useful for treating cancer and hypertension, comprises selecting a protein interacting with a target
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method of selecting a high-functioning protein
                                                                                                                                                                                                                                                                   GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCCAACTTGGCAGATGGGGTCCCATCA
                                                                                                                                                                    AGGITCAGTGGCAGTGGATCTGGCACAAATTITCTITCAAGATCAGCAGCCTACAGGCT
                                                                                                                                                       1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAGTGTCACC
                                                                                                                                                                                                                                                                                                                                                AGGTTCAGTGGTAGTGGATCTGGCACAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
                                                                                                                                                                                                                                                                                                                                                                               GAAGATITIGIAAATIATIACIGICAACAAGITITACAGITCICCATICACGITCGGIGCI
                                                                                                                           Gape
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              cytostatic; hypotensive; nucleic acid library; cancer; neoplasm; hypertension; cardiovascular disease; ds; gene.
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0
                                                                                           88.5%; Score 284.2; DB 3; Length 324; 92.8%; Pred. No. 7.5e-81; ive 0; Mismatches 23; Indels 0
                                                                   Sequence 324 BP; 86 A; 77 C; 78 G; 83 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       High-functioning protein related DNA SEQ ID NO 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; SEQ ID NO 110; 92pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                      GGGACCAAGCTGGAGCTGAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGACCAAGTTGGAAATAAAA 321
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                                                                                                                           Matches 298; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        standard; DNA;
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                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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                                                                                                                                                                                                                                                                                                             697 AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTTCCTTCAAGATCAGCACCTACAGGCT 756
                                                                                                                                                                                                                                                                                                                                                                   517 GACATCGAGCTCACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 576
                                                                                                                                                                                                            577 ATCACATGCCTCGCAAGTCAGACCATTGGTACATGGTTAGCATGGTATCAGCAGAAACCA 636
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                                                                                                                                                                                                                                                                                                                                                     GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCCATTCACGTTCGGTGCT 300
                                                                                                                           9
changes. This provides an advantage over current vaccines, as the virus periodically alters it's HA molecule
                                                                                                                          1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAAAGTGTCACC
                                                                                                                                                                                                                                                                                               181 AGGTICAGTGGCAGTGGATCTGGCACAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
                                                                                                                                                                                                                                         GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA
                                                                                                Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Changeable region of mouse monoclonal antibody recognizing surface antigen preS1 epitope of hepatitis B virus and gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        murine; surface antigen preS1 epitope;
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                                                                     Length 1228;
                                        0 Other;
                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  of the invention"
                                        Sequence 1228 BP; 362 A; 305 C; 282 G; 279 T; 0 U;
                                                                   Score 285.4; DB 2;
Pred. No. 5.3e-81;
0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KORE-) KOREA RES INST CHEM TECHNOLOGY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           324nt DNA sequence of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= a
/product= "Protein
                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure, Page 9; 14pp; Korean.
                                                                                                                                                                                                                                                                                                                                                                                                            GGGACCAAGCTGGAGCTGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BP
                                                                   Query Match
Best Local Similarity 93.4%;
Matches 298; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mouse monoclonal antibody; r
hepatitis B virus; gene; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ryoo CJ;
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which comprises constructing a protein-coding DNA library, transcribing DNAs, attaching a spacer to the 3' end of transcribed RNAs and constructing a library of molecules assigned to genotype and phenotype in a cell-free translation system, treating the library of assigned molecules, binding an assigned molecule to a target molecule and amplifying nucleic acid. The method is useful for selecting a high-functioning protein by selecting a protein interacting with a target molecule. The method is useful for manufacturing a protein which interacts with a target molecule. The single stranded antibodies are useful for treating cancer and hypertension. The method is rapid and efficient. The present sequence represents a high-functioning protein related DNA.
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Sequence 949 BP; 248 A; 218 C; 259 G; 224 T; 0 U; 0 Other;

	·;	09	611	120	671	180	731	240	791	300	851		
	Gарв	GTCACC	GTCATC	AAACCA	AAACCA	CCATCA	CCATCA	CAGGCT	CAGGCT				
949;	°,	AAAGT	AAAGT	AGCAG	AACAG	GGGTC	66610	GCCTA	GCCTA	CGTTC	CGTTC		
Length 949;	Indels	GACATTCAGATGACCCAGTCTCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCCCC		ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA		GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAATGGGGTCCCATCA		AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTTTTCAAGATCAGCAGCCTACAGGCT		GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT			
DB 14; 3e-80;	3 24;	STCTGCAT	STCTGCAT	ATGGTTAGG	ATGGTTAGG	CACCAACT	ACCAGCTO	FTCTTTCAZ	TCTTTCA	TACAGTTC	TACAGTAC		
Score 282.6; DB 1 Pred. No. 3.8e-80;	matche	CTCCCAC	CTCCCA	TGATAC	TGGTAC	TGCTGC	1-1-1-1 1-3-1-1-1-1-1-1-1-1-1-1-1-1-1-1-	AAAATT	AAAATT	ACAAGT	ACAACT		
Score 282.6; Pred. No. 3.86 0; Mismatches CTCCTGCCTCCCAG		TTCCTGC	AGACCAT	AGACCAT	TGATTTA	TGATTTA	CTGGCAC	TTGGCAC	ACTGTCA	ACTGTCA	AA 321	- AA 872	
88.0%; 92.5%; ive		ACCCAGI 		GCAAGTC GCAAGTC		CAGCTCC 		AGTGGAT AGTGGAT		AATTATT AGTTATT		GGGACCAAGCTGGAGCTGAAA 	
88. Jarity 92. Conservative		CAGATG CAGATG		recere recere		VICTOCT VITTOCT		AGTGGC		TTTGTA TTTGTA		PAGCTG	
Query Match Best Local Similarity		GACATI	GACATI			GGGAAA GGGAAA							
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Search completed: April 18, 2006, 18:33:15 Job time : 460 secs

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AL Submitted (1-NOV-2003) Masahira Hattori, The Institute of Physical and Chemical Research (RIKBN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa, 230-0045, Japan (E-mail:hattori@gsc.riken.jp, UKL:http://hgp.gsc.riken.go.jp/, Tel:81-45-503-9110, Fax:81-45-503-9170)
Clones are derived from the mouse BAC library MSMg01. For BAC library availability, please contact Kuniya Abe (abe@rtc.riken.jp). Tsukuba Institute of Physical and Chemical Research (RIKEN) 3-1-1 Koyadai, Tsukuba, 305-0074 Japan Chemical Research (RIKEN) 3-1-1 phone: 81-298-36-9189, fax: 81-298-36-9199
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AG319984 100 bp DNA linear GSS 18-DEC-2004 Mus musculus molossinus DNA, clone:MSMg01-105L04.T7, genomic survey
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AJ548351
UI-HF-BLO
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Contribution of Asian mouse subspecies Mus musculus molossinus to genomic constitution of strain C57BL/63, as defined by BAC-end sequence-SNP analysis
                                                                                                               UI-HF-BLO
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EST27109
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Mus musculus molossinus
Eukaryota; Metazoa; Chordata; Craniata, Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
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Hattori,M., Toyoda,A., Noguchi,H., Kojima,T. and Sakaki,Y.
Direct Submission
                                      BF580331
AW406886
AW405906
AW405906
AW405753
CD685478
CD685478
CD684441
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                                                                                                                                                                                 AJ548351
AM405753
AM405753
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BP421572
CD710582
CD55909
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: EcoRI
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R.Site 2
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Copyright (c) 1993 - 2006 Biocceleration Ltd.
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Contact: Shultz MA
Dept. of Molecular Biosciences, School of Veterinary Medicine
University of California, Davis
University of California, Davis
University of California, Davis
University of California, Davis
Tal: 530 752 0793
Fax: 530 752 4698
Fax: 530 752 4698
Fax: 530 752 4698
Fax: 500 752 4698
F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CF111270 603 bp mRNA linear EST 23-JUL-2003 Shultzomica04521 Rat lung airway and parenchyma cDNA libraries Rattus norvegicus cDNA clone Contig432 5', mRNA sequence. CF111270 CF111270.1 GI:33167972
                                                                                                                                                                                                                                                                                                                                                                       CCAGGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCA 177
          /clone_lib="NCI_CGAP_Mam5"
/note="Organ: mammary; Vector: pCMV-SPORT6; Site_1: Sall; Site_2: Not1; Cloned unidirectionally. Primer: Oligo dT. Library constructed by Life Technologies. Investigators providing samples: Lothar Hennighausen/Robin Humphreys, NIH"
                                                                                                                                                                                                                                                                                                                                                                                                                                            CA-TCACATGCCTGGCAAGTCAGACCATTGATACA-TGGTTAGCATGGTATCAGCAGAAA 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         286 GCTGAAGATTTTGTAACTTATTACTGTCAACAACGTTTACAGTACTCCCGTGGACGTTCGG 345
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Euteleostomi;
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Rattus norvegicus

Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi, Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi, Bammalia; Butheria; Buarchontoglires; Glires; Rodentia; Sciurcognathi; Muroidea; Murinae; Rattus.

1 (bases 1 to 603)

Shultz, M.A., Zhang, L., Gu, Y.-Z., Baker, G.L., Fannuchi, M.V., Padua, A.M., Gurske, W.A., Morin, D., Penn, S.G., Jovanovich, S.B., Plopper, C.G. and Buckpitt, A.R.

Gene expression analysis in response to lung toxicants: I. Sequencing and microarray development

L. Am. J. Respir. Cell Mol. Biol. 30 (3), 296-310 (2004)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            106 CAGTCACATGCCTGGCAAGTCAGACCATTGGTACACTGGTTAGCATGGTATCAGCAAGAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GCTGAAGATTTTGTAAATTATTACTGTCAACAA-GTTTACAGTTCTCCATTCACGTTCGG
                                                                                                                                                                                                                                                                                                                                       GACATTCAGATGACCCAG-TCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCAC
                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                  Length 553;
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                                                                                                                                                                                                                                     DB 2;
                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                  Score 248.2; DB 2
Pred. No. 1.9e-65;
0; Mismatches 18

    .603
/organism="Rattus norvegicus"
/mol_type="mRNA"

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/lab host="DH10B"
                                                                                                                                                                                                                                     77.3%;
                                                                                                                                                                                                                                                                                        303; Conservative
                                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    271 AGGTTCAGTGGTAGTGGATCTGGCACAAAGTTTTCTTTCAAGATCAGGCGCTACAGGCT
                                                                                                                                                                                                                                                                                                                                                                  1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTTGGGAGAAGTGTCACC
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                                                                                                                                                                                                                                                                Length 700;
                     /mol_type="genomic DNA"
fub species="molossinus"
fub xref="taxon:57486"
/clone="MSMg01-105L04.T7"
fexx="male"
flasue type="mixture of kidney and spleen"
/clone_libe"MSMg01 Mouse Male BAC Library"
                                                                                                                                                                                                                                                                                                              Indels
  'organism="Mus musculus molossinus"
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/strain="mix FVB/N, C57BL/6J"
/db_xref="taxon:10090"
/clone="IMAGE:3486245"
/tissue_type="tumor, gross tissue"
/dev_stage="7 months"
                                                                                                                                                                                                                                                          Score 270.8; DB 10;
Pred. No. 2.1e-72;
0; Mismatches 12;

    .553
    /organism="Mus musculus"

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BE309991
BE309991.1 GI:9169034
                                                                                                                                                                                                                                                             Query Match
Best Local Similarity 95.9%;
Matches 278; Conservative
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                                                                           /tissue_type="airway or parenchyma"
/dev_stage="adult"
/clone_lib="Rat lung airway and parenchyma cDNA libraries"
/note="Organ: lung, Vector: pGBM-112f(-); Site_1: Eco RI;
Site_2: Not I; mRNA was isolated from microdissected rat
lung_airways and parenchyma tissues."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       mRNA linear EST 12-JUN-2001 musculus cDNA clone IMAGE:4971397
                                                                                                                                                                                                                                                                                                                                                                                               119
                                                                                                                                                                                                                                                                                                                                          GACATCCAGATGACACAGTCTCCTGGCCTCCTGTCTGCATCTCTGGAAGAAATTGTCAC 100
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Mus musculus
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Bukaryota; Metazoa; Chordata; Craniata; Sciuregnathi; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidea; Muridae; Mus.
1 (bases 1 to 896)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Robert Strausberg, Ph.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
Email: cgapbe-r@mail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://mage.lln.gov
Plate: LLAM10956 row: k column: 14
High quality sequence stop: 864.
                                                                                                                                                                                                                                                                                                                                                                                                                     101 GATCACATGCCAGGCAAGCCAGGACATTGGTAATTGGTTAACATGGTATCAGCAGAAACC
                                                                                                                                                                                                                                                                                                               GACATTCAGATGACCCAGTCTCCT-GCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCAC
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                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                               1;
                                                                                                                                                                                                                                  73.8%; Score 237; DB 6; Length 603;
llarity 85.4%; Pred. No. 5.9e-62;
Conservative 0; Mismatches 46; Indels
/strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="Contig432"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Mus musculus"
/mol_type="mRNA"
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                                                           /sex="male"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           mRNA sequence.
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Matches 275; Conser
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BG969371
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Mus musculus adult male kidney cDNA, RIKEN full-length enriched library, clone:0610010P20 product:immunoglobulin kappa chain AK002514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   240
/db_xref="taxon:10090"
/clone="IMAGE:4971397"
/lab_host="DH10B (TI phage-resistant)"
/clone=lib="NCI CGAP_Kid14"
/note="Organ: kidney; Vector: pCMV-SPORT6; Site_1: NotI; Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT. Average insert size 1.75 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library. |"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          79 GACATCCAGATGACTCAGTCTCCAGCCTCCCTATCTGTATCTGTGGGAGAAACTGTCACC 138
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AK002514.
AK002514.
TI GI:12832550
MUS musculus (house mouse)
Mus musculus
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontoglires; Glires; Rodentia;
Sciurognathi; Muridae; Murinae; Mus.
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                                                                                                                                                                                                                                                                                                                                            DB 2; Length 896;
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                                                                                                                                                                                                                                                                                                                                     Score 229.8; DB 2
Pred. No. 1.1e-59;
0; Mismatches 57
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High-efficiency full-length cDNA cloning
Meth. Enzymol. 303, 19-44 (1999)
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                                                                                                                                                                                                                                                                                                                                     71.6%;
82.2%;
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Fukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciutognathi; Muroidea; Murinae; Mus.

1 (bases 1 to 964)

2 NIH-MGC http://mgc.nci.nih.gov/.

3 NIH-MGC http://mgc.nci.nih.gov/.

4 Unpublished (1999)

5 Contact: Robert Strausberg, Ph.D.

6 Email: cgapbs-r@mail.nih.gov

7 Tissue Procurement: Jeffrey E. Green, M.D.

6 CDNA Library Preparation: Life Technologies, Inc.

6 CDNA Library Preparation: Life Technologies, Inc.

7 Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

7 http://image.llnl.gov

8 Plate: LLAMI0998 row: o column: 19

8 High quality sequence stop: 826.
VYAATNLADGVPSRFSGSGSGTQYSLKINSLQSEDFGSYFCQHFWGTPRTFGGGTKLE
IKRADAAPTVSIFPPSSEQLTSGGASVVCFLNNFYPKDINVKWKIDGSERQNGVLNSW
TDQDSKDSTYSMSSTLTLTKDBYERHNSYTCEATHKTSTSPIVKSFNRNEC"
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602832780F1 NCI_CGAP_CO24 Mus musculus cDNA clone IMAGE:4987626 5',
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                                                                                                                                                                                                                                                                   tch 70.6%; Score 226.6; DB 4; al Similarity 81.6%; Pred. No. 1.1e-58; 262; Conservative 0; Mismatches 59;
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/organism="Mus musculus"
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/clone="IMAGE:4987626"
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                                                                                                                                                                                     /note="putative"
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S Adachi, J., Aizawa, K., Akahira, S., Akimura, T., Arai, A., Aono, H., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Fukunishi, Y., Fukunishi, Y., Fukunio, M., Hanagaki, T., Hara, A., Hayatuu, N., Hiramoto, K., Huizoka, T., Hori, F., Imotani, Y., Itoh, M., Itoh, M., Izawa, M., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kono, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Okzaki, Y., Okido, T., Owa, C., Salto, H., Salto, R., Sarai, C., Sakai, Y., Sano, H., Sasaki, D., Shibata, K., Shibata, Y., Shinagawa, A., Shiraki, T., Sogabe, Y., Suzuki, H., Tagami, M., Tagawa, A., Takahsshi, F., Tanaka, T., Yoshino, M., Muramatsu, M. and Hayashizaki, Y., Poshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Toya, T., Yammura, T., Yasunishi, A., Yoshida, K., Yoshino, M., Muramatsu, M. and Hayashizaki, Y. Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 11-7-22 Sushiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-resegger.riken.jp, URL:bttp://genome.gec.riken.jp/, Tell:Bl-45-503-9222, Proceedicts of Markin Markin Markin M., Muramatsu, M., M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Please visit our web site (http://genome.gsc.riken.jp/) for further
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/dev_stage="adult"
101._.736
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/note="unnamed protein product; immunoglobulin kappa chain
variable 28 (V28) (LocusLink|16114, GB|AK002514, evidence:
BLASTN, 100*, match=939)
                                                                                                                                                                                                                                                                                                                                                                                   Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
                                                                                                                                                                               The RIKEN Genome Exploration Research Group Phase II Team and the ANTOM Consortium.
Functional annotation of a full-length mouse cDNA collection Nature 409, 685-690 (2001)
                                                                                                                                                                                                                                                                                                                       The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
   Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y. RIKRN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer Genome Res. 10 (11), 1757-1771 (2000)
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db_xref="taxon:10090"
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6 (bases 1 to 939)
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602833496F1 NCI_CGAP_Co24 Mus musculus cDNA clone IMAGE:4988038 5',
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S NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Lupublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

CDNA Library Preparation: Life Technologies, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Incyte Genomics, Inc.

Clone distribution: MGC. clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:

http://image.llnl.gov

Plate: LLAM10999 row: p column: 23

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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia,
Sciurognathi, Muroidea, Muridae, Murinae, Mus.
       Stem cell origin."
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/cloh bost="DHIOB"
/cloh bla="NCI CAAP Lu29"
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Site_2: Not1; Cloned unidirectionally. Primer: Oligo d
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NHH"
                                                                                                                                                                                                                                                                                                                                                                                                           236 AGGTTCAGTGGCAGTGGATCAGGCACACAGTTTTCTCTGAAGATCAACAGCCTGCAGCCT
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0; Mismatches 62; Indels 0
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/organism="Mus musculus"
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Matches 259; Conservative
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BG967689
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                                                                                                                                                                                                                                        /lab_host="DH10B (Tl phage-resistant)"
/clone_lib="NCI_CGAP_Co24"
/note="Corgan: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: Sall; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
                                                                                                                                                                                                                                                                                          ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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/clone="IMAGE:3492034"
/tissue_type="spontaneous tumor, metastatic to mammary.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AGGTTCAGTGGCAGTGGATCAGGCACACAGTTCCCTCAAGATCAACAGCCTGCAGTCT
                                                                                                                                                                                     Gaps
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0
                                                                                                                                                  Length 964;
                                                                                                                                                                                    59; Indels
                                                                                                                                             Score 226.6; DB 2;
Pred. No. 1.1e-58;
0; Mismatches 59;
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/mol_type="mRNA"
/strain="Czech II"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GGCACCAAGCTGGAAATCAAA 396
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BE305476.1 GI:9157223
                                                                                                                                              tch 70.6%; al Similarity 81.6%; 262; Conservative 0
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Siii (ggccattatgcc); Site 2: Siii (ggccatctgcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGCCATATGGCC-3' and 3' adaptor sequence:
5'-ATCTAGAGGCGACGCGCACTG-dT(30) BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Palo Alto,
CA). Note: this is a NIH_MGC Library."
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CH230-317B9.TV CHORI-230 Segment 2 Rattus norvegicus genomic clone
CH230-317B9, genomic survey sequence.
BZ120378
    note="Organ: Pooled-Glandular; Vector: pDNR-LIB; Site_1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        99 GACATCCAGATGACCCAGTCTCCATCCTCCTCTGCATCTGTAGGAGACAGAGTCACC 158
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Rattus norvegicus
Eukaryota; Metacoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia;
Sciurognathi; Muroidae; Muridae; Rattus.
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Rat BAC End Sequences from Library CHORI-230 Mbol segment Unpublished (1999)
Other_GSSs: CH230-317B9.TJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAGTGTCACC
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Clones are derived from the rat BAC library CHORI-230
(http://www.chori.org/bacpac/rat230.htm). For BAC library
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Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
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BZ120378.1 GI:23761325
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Matches 259; Conservative
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Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits
CDNA Library Preparation: CLONTECH Laboratories, Inc.
CDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: NDCM133 row: h column: 21
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/lab_host="DH10B (TI phage-resistant)"
/clone_lib="NCI CGAP_Co24"
/note="Organ: colon; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dT.
Average insert size 1.6 kb. Constructed by Life
Technologies. Note: this is a NCI_CGAP Library."
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1 (bases 1 to 797)

11 HWGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
                                                                                                                                                                                                                                                                                         1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAGTGTCACC
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TMAGE:30326300 5', mRNA sequence.
                                                                                                                                                                                             Length 721;
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/mol_type="mRNA"
/db_xref="texon:9606"
/clone="IMAGE:30326300"
/lab_host="DH108 (T1 phage-resistant)"
/clone_lib="NIH_MGC_184"
                                                                                                                                                                                             Query Match 69.1%; Score 221.8; DB 2; Best Local Similarity 80.7%; Pred. No. 3.2e-57; Matches 259; Conservative 0; Mismatches 62;
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Location/Qualifiers
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Homo sapiens
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Buarchontcglires; Glires; Rodentia;
Sciurognathi; Murcidea; Muridae; Murinae; Mus.
1 (bases 1 to 599)
Solurognathi; Murcidea; Muridae; Mus.
1 (bases 1 to 599)
Solurognathi; Musc. nci.nih.gov.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbarsemilinh.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.B. Consortium/LLNL at:
availability, please contact Pieter de Jong (pdejong@mail.cho.org). Clones may be purchased from BACPAC Resources (http://www.chori.org/bacpac/or ering information.htm). BAC end page: http://www.tigr.org/tdb/bac_ends/rat/bac_end_intro.html Plate: 317 row: B column: 9 Seq primer: T7 Class: BAC ends.
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                                                                                                                                                                                                                              /db_xref="taxon:10116"
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CHORI-230 Rat (BN/SsNHsd/MCW) BĀC library produced by Pieter de Jong"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC
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Pred. No. 4.9e-57;
0; Mismatches 43; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  43; Indels
                                                                                                                                                      1. .727
/organism="Rattus norvegicus"
                                                                                                                                                                                            /mol_type="genomic DNA"
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                                                                                                                                     Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EST.
Mus musculus (house mouse)
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BE287315.1 GI:9166132
                                                                                                                                                                                                                                                                                                                                                                                                                           68.9%;
85.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local Similarity 85.2'
Matches 247; Conservative
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ORGANISM
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TITLE
JOURNAL
COMMENT
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VERSION
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BE287315
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Hominidae; Homo.

1 (Dases 1 to 683)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)

Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Dr. Michael Brownstein and Dr. Miklos Palkovits

CDNA Library Preparation: CLONTECH Laboratories, Inc.

CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LIML)

DNA Sequencing by: Agencourt Bioscience Corporation

Clone distribution: MGC clone distribution information can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST 01-MAY-2003
                                                                                                                                                                                         /db_xref="taxon:10090"
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Mammalia; Eutheria; Buarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     247 AGATTCAGTGGCAGTGGATCAGGCACACAGTATTCCCTCACGATCAACAGCCTGCAGTCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 220.2; DB 2; Length 599;
Pred. No. 9.4e-57;
0; Mismatches 63; Indels 0
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Plate: LLAM8528 row: k column: 21
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Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 258; Conservative
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                     Email: cgapbs.romail.nih.gov
Tissue Procurement: Lothar Hennighausen Ph.D., Robin Humphreys
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC.clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMSS3 row: i column: 16
High quality sequence stop: 568.
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IMAGE:7375130 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           68.6%; Score 220.2; DB 2; Length 691;
80.4%; Pred. No. 9.8e-57;
ive 0; Mismatches 63; Indels 0;
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    .691
    /organism="Mus musculus"

     Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NIH-MGC http://mgc.nci.nih.gov/
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Rattus norvegicus
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Matches 258; Conservative
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AUTHORS
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     COMMENT
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                                                                                                                                                                                                                           /d.zter="InAGE:3025948"
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/lab_host="MINGE 13025948"
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Sfil (ggccattatggcc); Site_2: Sfil (ggccgctcggcc);
Library is oligo-dT primed and directionally cloned. cDNA
was prepared from a glandular pool of tissues from thyoid,
parathyroid, adrenal, cortex and pineal gland. 5' and 3'
adaptors were used in cloning as follows: 5' adaptor
sequence: 5'-CACGGCGATTATGGCC-3' and 3' adaptor sequence:
5'-ATTCTAGAGGCGGGGGGGGCGATG-GT(30)BN-3' (where B = A,
C, or G and N = A, C, G, or T). Average insert size 1.38
kb (range 0.60-3: S.kb). 15/15 colonies contained inserts
by PCR. This library was enriched for full-length clones
and was constructed by Clontech Laboratories (Falo Alto,
CA). Note: this is a NIH_MGC Library."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AGGTTCAGTGGCAGTGGATCTGGCACAAATTTTTCAAGATCAGCAGCCTACAGGCT 240
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1. (bases 1 to 691)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Plate: NDCM132 row: j column: 05
High quality sequence stop: 547.
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                                                                                                                                                       /organism="Homo sapiens"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          390 GGACCAGGGTGGAGATCAAA 410
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TITLE
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Gaps

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251

240

180

EST 19-JUL-2004

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/MOL type="mRNA"
/db xref="taxon:9606"
/clone="INAGE:4854409"
/tlssue type="primary B-cells from tonsils (cell line)"
/tlssue type="primary B-cells from tonsils (cell line)"
/tlssue type="primary B-cells from tonsils (cell line)"
/clone="Drigat: B-cells, Vector: pOTB7; Site_1: Xho1;
Site_2: ECORI; cDNA made by oligo-dT priming.
Directionally cloned into EcORI/Xho1 sites using the
following 5' adaptor: GGCAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by Ling
Hong in the laboratory of Gerald M. Rubin (University of
California, Berkeley) using ZAP-CDNA synthesis kit
(Stratagene) and Superscribt II RT (Life Technologies).
Note: this is a NIH_MGC Library."
                                                                                                                                                                                                 Hominidae; Homo.

E 1 (bases 1 to 867)

S NIH-MGC http://mgc.nci.nih.gov/.

I (bases 1 to 867)

S NIH-MGC http://mgc.nci.nih.gov/.

L Unpublished (1999)

Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Louis M. Staudt, M.D., Ph.D.

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Hong/Rubin Laboratory

CDNA Library Preparation: Ling Genomics, Inc.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LiNL at:

http://image.llnl.gov

Plate: LiCM1702 row: a column: 02

High quality sequence stop: 805.

Location/Qualifiers
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Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    85 GCCATCCAGTTGACCCCAGTCTCCCTGTCTGTCTGTAGGAGACAGAGTCACC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Homo sapiens"
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                                                                            Homo sapiens (human)
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Matches 258; Conserv
             3G754732.1
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// (db_xref="taxon:10116"
// (db_xref="taxon:10116"
// (db_xref="taxon:10116"
// (do_xref="taxon:10116"
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602714301F1 NIH_MGC_48 Homo sapiens CDNA clone IMAGE:4854409 5',
MRNA sequence.
BG754732
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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                                                       Contact: Daniela S. Gerhard, Ph.D.

Contact: Daniela S. Gerhard, Ph.D.

Office of Cancer Genomics
National Cancer Institute / NIH

Bldg. 31 RmloAD/Betheda, MD 20892

Email: Gapbs-remail.inh.gov
Tissue Procurement: Drs. Josef Lazar & Howard Jacob, Medical
College of Wisconsin

CDNA Library Preparation: Open Biosystems
CDNA Library Preparation: Open Biosystems
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMISSSS row: b column: 24
High quality sequence stop: 632.

Location/Qualifiers
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      National Institutes of Health, Mammalian Gene Collection (MGC)
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Pred. No. 1e-56;
0; Mismatches 63;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Rattus norvegicus"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity 80.4%;
Matches 258; Conservative (
                                      Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61
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TITLE
JOURNAL
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Sequence 3, Sequence 8, Patent No. 52 Sequence 62, Sequence 1,

Sequence

Appli Appli Appli Appli Appli Appli Appli Appli Appli

Sequence 1, A Sequence 5, A Sequence 11, Sequence 2, A Sequence 1, A Sequence 1, A Sequence 8, A

Appli Appli Appli Appli Appli

Sequence Sequence

Sequence 13, Assequence 3, Assequence 3, Assequence 3, Assequence 3, Assequence 1, Ass

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Sequence 1, Application US/08814806
| Patent No. 598605
| GENERAL INFORMATION:
| APPLICANT: Mong, Hing C. |
| APPLICANT: Lawrence, Luepschen |
| TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD |
| TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD |
| TITLE OF INVENTION: COAGULATION AND METHODS OF USE THEREOF |
| NUMBER OF SEQUENCES: 26 |
| CORRESPONDENCE ADDRESS: |
| ADDRESSEE: Dike Bronstein, Roberts & Cushman, LLP |
| STREET: 130 Water Street |
| CITY: Boston |
US-08-378-939-33
US-08-230-843-3
US-08-230-843-3
US-08-770-916-3
US-09-770-916-3
US-08-792-824-8
US-09-996-1
US-08-792-824-1
US-08-792-824-1
US-08-792-824-1
US-08-792-824-1
US-08-792-824-1
US-08-792-824-1
US-08-792-824-1
US-09-897-511A-13
US-09-897-511A-13
US-09-767-888-3
                                                                                                                                                                                                                                                                  PCT-US94-07659-3
                                                                                                                                                                                                                                                                                                         ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/814,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: INFORMATION:
NAME: COLIEGS, PECEF F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
  COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: CDNA HYPOTHETICAL: NO
    US-08-814-806-1
 sequence 34, Appli
Sequence 7, Appli
Sequence 22, Appli
Sequence 22, Appli
Sequence 21, Appl
Sequence 22, Appl
Sequence 22, Appl
Sequence 21, Appl
Sequence 21, Appl
Sequence 21, Appl
                                                                                     April 18, 2006, 18:26:07 ; Search time 167 Seconds (without alignments) 3416.750 Million cell updates/sec
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Sequence 1, Appli
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Sequence 35,
Sequence 34,
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                                                                                                                                                                   1 gacattcagatgacccagtc......ggaccaagctggagctgaaa 321
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Sequence 1
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Sequence 1
            GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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/cgn2_6/ptodata/1/ina/5_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/6_COMB.seq:*
/cgn2_6/ptodata/1/ina/H_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCOMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/PP_COMB.seq:*
/cgn2_6/ptodata/1/ina/RB_COMB.seq:*
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US-09-647-468-13
US-09-641-908-35
US-08-401-908-35
US-08-401-908-4-7
US-09-140-084-22
US-09-140-084-22
US-09-724-297-21
US-09-724-108-22
US-09-724-108-23
US-09-724-108-24
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US-08-378-939-31
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Maximum Match 100%
Listing first 45 summaries
                                                             OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Query
Match Length DB
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321
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Sequence 12, Application US/09647468

| Sequence 12, Application US/09647468
| Patent No. 6677436
| GENERAL INFORMATION:
| APPLICANT: SATO, KOH
| APPLICANT: ADACHI, HIDEKI
| APPLICANT: TABUTA, NACHIRO
| TITLE OF INVENTION: HUMANIZED ANTIBODY ACAINST HUMAN TISSUE FACTOR (TF) AND
| TITLE OF INVENTION: HUMANIZED ANTIBODY
| FILE REFERENCE: 053466/0289
| CURRENT FILING DATE: 2000-09-29
| CURRENT FILING DATE: 1999-04-02
| PRIOR FILING DATE: 1999-04-02
| PRIOR FILING DATE: 1998-14-03
| NUMBER OF SEQ ID NOS: 183
| SOFTWARE: PATENTIN VEY: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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NAME/KEY: mat_peptide
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                                                                                                                                                                                                                                                                                                                                  Length 321;
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                                                                                                                                                                                                                                                                                                                                Query Match 100.0%; Score 321; DB 3; Best Local Similarity 100.0%; Pred. No. 1.2e-96; Matches 321; Conservative 0; Mismatches 0;
                                       TYPE: nucleic acid
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
FRAGMENT TYPE: «Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GGGACCAAGCTGGAGCTGAAA 321
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS.
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LENGTH: 375
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GAAGATTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
                                                                                                                                                                                                                                                                                                                                                                                                            GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                      121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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EAWTENCE, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 26
                                                                                                                   Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
                                                                                                                                                                  Indels
                                                                                                                                                                  ö
                                                                                                                 Query Match
100.0%; Score 321; DB 2;
Best Local Similarity 100.0%; Pred. No. 1.2e-96;
Matches 321; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:

MEDIUM TYPE: Diskerte

COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS

SOFTWARE: FastSEQ Version 1.5

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/293, 854

FILING DATE: 16-Apr-1999

CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: COTIESS, PETER F
REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46943
TELEPHONE: 617-523-3400
TELEPHONE: 617-523-6440
TELEEX: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/814,806
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           301 GGGACCAAGCTGGAGCTGAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         301 GGGACCAAGCTGGAGCTGAAA 321
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Patent No. 6555319
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Jiao, Jin-an
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, B
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
                      ; FRAGMENT TYPE:
; ORIGINAL SOURCE:
US-08-814-806-1
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RESULT 2
US-09-293-854-1
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180
                                                                                                                                     115 ATCACATGCCTGGCAAGTCAGACCATTGGTACATGGTTAGCCTGGTATCAGCAGAAACCA 174
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                                                                                                                                                                                                                                     175 GGGAAATCTCCTCAGGTCCTGATTTATGCTGCAACCAGCTTGGCAGATGGGGTCCCATCA 234
                                                                                                                                                                                                                                                                                                                                                                          241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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WESULT 5

Sequence 35, Application US/08401908

Sequence 35, Application US/08401908

FILED OF SEATION: YOSHINODU OKUNO et al.

APPLICANT: YOSHINODU OKUNO et al.

TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF TITLE OF INVENTION: ANTIBODY

NUMBER OF SEQUENCES: 36

CORRESPONDENCES: 36

CORRESPONDENCES: 36

CONFUER: Wendercth, Lind & Ponack STREET: Weshington Street, N.W., #700

CITY: Weshington

STATE: D.C.

COUNTRY: U.S.A.

ZIP: 20005

STATE: D.C.

COMPUTER: READABLE FORM:

MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb

COMPUTER: IN COMPUTER: MS.

MEDIUM TYPE: Diskette, 5.1

COMPUTER: Wordperfect 5.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/401,908

FILING DATE: MARCH 10, 1995

CLASSIFICATION NUMBER:

PRIOR APPLICATION NUMBER:

FILING DATE:

APPLICATION NUMBER:
                                     GGGAAATCTCCTCACTCCTCGTTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA
                                                                                                                                                                                                                                                                                                           1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC
                                                                                                    ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                                                 181 AGGTTCAGTGGCAGTGGATCTGGCACAAATTTTTTTTTCAAGATCAGCAGCCTACAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GGGACCAAGCTGGAAATAAAA 375
                                                                                                                                                                                                                                                                                                                                                                                                                                                                301 GGGACCAAGCTGGAGCTGAAA 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REGISTRATION NUMBER: 33,367
REPERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-8850
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       35:
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SEQUENCE CHARACTERISTICS:
LENGTH: 1228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      nucleic acid
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STRANDEDNESS: dou
TOPOLOGY: linear
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                                                                                                                                                                                                                                  GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181 AGGTTCAGTGGCAGTGGGTTCTGGCACAAAATTTTCTAGAATCAGGCAGCCTACAGGCT 240
                                                                                                                                                                                                                                                                                                                                                                                                               235 AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 294
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (TF) AND
                                                                                                                                                                                                         1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 13, Application US/09647468

Patent No. 6677436

GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACH, HIDEKI
APPLICANT: YABUTA, MOGHIRO
TITLE OF INVENTION: HUMANIZED ANTHEODY AGAINST HUMAN TISSUE FACTOR (TF) A;
TITLE OF INVENTION: HUMANIZED OF PRODUCTION OF THE HUMANIZED ANTHEODY
TITLE OF INVENTION: HUMBER: US/09/647,468
FILE REFERENCE: 053466/0289
CURRENT FILING DATE: 1999-29
PRIOR FILING DATE: 1999-04-02
PRIOR PLING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 13
                                                                                                                                                                   Gaps
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NAME/KEY: sig_peptide
LOCATION: (1) .. (54)
NAME/KEY: mat_peptide
LOCATION: (155) .. (575)
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                                                                                                             Query Match
91.5%; Score 293.8; DB 3; Length 375;
Best Local Similarity 94.7%; Pred. No. 1.4e-87;
Matches 304; Conservative 0; Mismatches 17; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 375;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          301 GGGACCAAGCTGGAGCTGAAA 321
; LOCATION: (55)..(375)
; NAME/KEY: CDS
; LOCATION: (1)..(375)
US-09-647-468-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; LOCATION: (1)..(375)
US-09-647-468-13
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                                                                                                                                                                                                                                                                                                                                          AGGTTCAGTGGCAGTGGATCTGGCACAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
                                                         61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA
                                                                                                                                                                                                                                                     AGGTTCAGTGGTAGTGGATCTGGCACAAAATTTTCCTTCAAGATCAGCAGCCTACAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 7, Application US/07789344A
| Sequence 7, Application US/07789344A
| Patent No. 5318897
| GENERAL INRORMATION:
| APPLICANT: Sudhir: Paul
| TITLE OF INVENTION: WONOCLONAL ANTIBODY AND ANTIBODY
| TITLE OF INVENTION: COMPONENTS ELICITED TO A POLYPEPTIDE ANTIGEN
| TITLE OF INVENTION: GROUND STATE
| NUMBER OF SEQUENCES: 13
| CORRESPONDENCE ADDRESS:
| ADDRESSEE: Clutis, Morris & Safford
| CITY: New York
| STATE: New York
| COUNTRY: United States of America
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 GACATTCAGATGACCCCAGTCTCCTGCCTCTCTGCATCTCTGGGAGAAGTGTCACC
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CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/01/189,344A
FILING DATE: 08-NOV-1991
CLASSIFICATION: 435
ATTONEY/AGENT INFORMATION:
NAME: Evans, Barry
REGISTRATION NUMBER: 22,802
REGISTRATION NUMBER: 370068-3500
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELEPHONE: (212) 840-3333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 86.7%; Score 278.4; DB 2; Best Local Similarity 93.3%; Pred. No. 1.7e-82; Matches 291; Conservative 0; Mismatches 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                   GGGACCAAGCTGGAGCTGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                GCACCAAGCTGGAGTCGA 907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEPHONE: (212) 840-3333
TELEFAX: (212) 840-0712
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 312 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear
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                                                                               577 ATCACATGCCTGGCAAGTCAGACCATTGGTACATGGTTAGCATGGTATCAGCAGAAACCA 636
                                                                                                                                                                 181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
                                                                                                                                                                                                                                                                                                                                          517 GACATCGAGCTCACCCAGTCTCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 576
                                                         61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
                                                                                                                                           121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                                                                                                                                                                                                                                                                                 241 GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
                                                                                                                                                                                                                                                     AGGTTCAGTGGTAGTGGATCTGGCCACAAAATTTTCCTTCAAGATCAGCAGCCTACAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 34, Application US/08401908

Sequence 34, Application US/08401908

GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: ANTIBODY
TITLE OF INVENTION: ANTIBODY
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Washington
STATE: D.C.
COUNTRY: U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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89.4%; Score 287; DB 2; Length 1300;
Best Local Similarity 93.7%; Pred. No. 4.5e-85;
Matches 299; Conservative 0; Mismatches 20; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,908
FILING DATE: March 10, 1995
CLASSIFICATION NUMBER:
ATTORNEY/AGENT INFORMATION:
NAME: Warren M. Cheek, Jr.
REFERENCE/DOCKET NUMBER: 33.367
REFERENCE/DOCKET NUMBER: 33.367
REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX:
TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                   301 GGGACCAAGCTGGAGCTGA 319
                                                                                                                                                                                                                                                                                                                                                                                                                                           817 GCCACCAAGCTGGAGTCGA 835
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SEQUENCE CHARACTERISTICS:
LENGTH: 1300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear
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Sequence 22, Application US/09140084A
Patent No. 6300065
GENERAL INFORMATION:
APPLICANT: Kieke, et al.
TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
FILE REFERENCE: D6661C1P2
CURRENT APPLICATION UNDBER: US/09/140,084A
CURRENT FILING DATE: 1998-08-26
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PatentIN Ver. 2.0
SEQ ID NO 22
LENGTH: 366
                                                                                                                                                           GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCGAGAAAGTGTCACC 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GACGTCCTGGTGACTCCTGCCTCCTGTCTGCATCTCCGGATGAATCTGTCACC 60
    61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA
                                                                                                61 ATCACATGCCTGGCAAGTCAGACCATTGGTACATGGTTAGCATGGTATCAGCAGAAACCA
                                                                                                                                                                                           121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCAACCAGCTTGGCAGATGGGGTCCCATCA
                                                                                                                                                                                                                                                 AGGTTCAGTGGCAGTGGATCTGGCACAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
                                                                                                                                                                                                                                                                                     181 AGGTTCAGTGGTAGTGGGATCTGGCACAAATTTTCCTTCAAGATCAGCCTACAGGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                181 AGGTTCAGTGGCAGTAGATCTGGCACACAGTATTCTCTTAAGATCAACAGACTACAGGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCCATTCACGTTCGGTGCT
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                                                                                                                                                                                                                                                                                                                                                    241 GAAGATTTGTAAGTTATTACTGTCAACAACTTTACAGTACTCCGTGGACGTTCG 295
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                                                                                                                                                                                                                                                                                                                                  GAAGATITIGIAAATIATIACIGICAACAAGITITACAGITICICCATICACGITICG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     74.6%; Score 239.4; DB 3; 84.1%; Pred. No. 1.7e-69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 10
US-09-140-084-23
; Sequence 23, Application US/09140084A
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ORGANISM: Artificial Sequence
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                                          ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
GACATTGTGCTGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC 60
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Sequence 4, Application US/08401908
Patent No. 568446
GENERAL INFORMATION:
APPLICANT: Yoshinobu OKUNO et al.
TITLE OF INVENTION: A DNA WHICH CODES FOR THE VARIABLE REGION OF TITLE OF INVENTION: ANTIBODY
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Wenderoth, Lind & Ponack
STREET: 805 Fifteenth Street, N.W., #700
CITY: Mashington
STATE: D.C.
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86.4%; Score 277.4; DB 2; Length 295;
Best Local Similarity 96.3%; Pred. No. 3.6e-82;
Matches 284; Conservative 0; Mismatches 11; Indels 0
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MEDLUM TYPE: Diskette, 3.5 inch, 1.44 mb
MEDLUM TYPE: Diskette, 3.5 inch, 1.44 mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/401,908
FILING DATE: March 10, 1995
CLASSIFICATION 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: FILING DATE:
ATTING DATE:
ATTING DATE:
ATTING DATE:
ATTING DATE:
TELECOMMUNICATION WHERE:
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INPORMATION:
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Best Local Similarity 84.1%; Pred. No. 1.7e-
Matches 270; Conservative 0; Mismatches
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US-09-724-297-22
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LENGTH: 366
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; Sequence 21, Application US/09724297
; Patent No. 642538
; GENERAL INFORMATION:
; APPLICANT: The Board of Trustees of the University of Illinois
; APPLICANT: Witting, et al.
; APPLICANT: Witting, et al.
; TITLE OF INVENTION:
; FILE REFERENCE: 97-99C
; CURRENT APPLICATION NUMBER: US/09/724,297
; CURRENT PILING DATE: 2000-11-28
; PRIOR FILING DATE: 1998-01-20
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: Patentin version 3.0
; SEQ ID NO 21
: LENGTH: 366
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                              APPLICANT: Kieke, et al.

TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof FILE REFERENCE: D6061CIPD.

CURRENT APPLICATION NUMBER: US/09/140,084A

CURRENT FILING DATE: 1998-08-26

NUMBER OF SEQ ID NOS: 26

SEQ ID NO 23

LENGTH: 366
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                                                                                                                                                                                                                      FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:PCR products
OTHER INFORMATION: KJ16-mut4
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                                                                                                                                                                                                                                                                                                               Length 366;
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NAME/KEY: misc feature

LOCATION: ()...()

COTATION: (>...()

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COTATION: (>...()

COTATION: PCR products of wild type scFv-KJ16

US-09-724-297-21
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                GENERAL INFORMATION:
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DB 3; Length 366;

74.6%; Score 239.4;

Query Match

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Sequence 22, Application US/09724297

Patent No. 6423538
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: Wittin, teast Call Surface Display of Proteins and Uses Thereof CURRENT FILING DATE: 2000-11-28
RIOR APPLICATION NUMBER: US 09/009,388
PRIOR APPLICATION NUMBER: US 09/009,388
PRIOR PILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: Patentin version 3.0
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1.7e-69;
ches 51;
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181 AGGITCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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Patent No. 6699658
GENERAL INFORMATION:
TITLE OF INVENTION: Yeast Cell Surface Display of Proteins
TITLE OF INVENTION: and Uses Thereof
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: McGREGOR & ADLER, LLP
                                                                                                                                                                                                                                                                                                                                                                                                    51; Indels
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                                                                                                                                                                                                                                                         ; LOCATION: ()...(); OTHER INFORMATION: PCR products of KJ16-mut4US-09-724-108-22
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COMPUTER READABLE FORM:
MEDIUM TYPE: 1.44 Mb floppy disk
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Apple Macintosh
COMPUTER: Office 98
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/009,388C
FILING DATE: 20 JAN 1998
CLASSIFFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/866,398
FILING DATE: 30 MAY 1997
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: Houston STATE: LEP STREET: 8011 Candle Lane CITY: Houston STATE: Texas COUNTRY: USA
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  CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/()
PRIOR FILING DATE: 1998-01-20
NUMBER OF SEQ ID NOS: 26
SOFTWARE: PATENTIN VERSION 3.0
SEQ ID NO 22
LENGTH: 366
                                                                                                                                                                   TYPE: DNA ORGANISM: artificial sequence
                                                                                                                                                                                                                                      NAME/KEY: misc feature
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US-09-009-388C-21
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Patent No. 6696251
GENERAL INFORMATION:
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: Witrup, et al.
ITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
FILE REFERENCE: 97-990
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Patent No. 6696251
GENERAL INFORMATION:
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: Wittrup, et al.
TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
FILE REFERENCE: 97-99
CURRENT APPLICATION NUMBER: US/09/724,108
GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
                          61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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74.6%; Score 239.4; DB 3; Length 366;
Best Local Similarity 84.1%; Pred. No. 1.7e-69;
Matches 270; Conservative 0; Mismatches 51; Indels 0
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; CHER INFORMATION: PCR products of wild type scFv-KJ16
US-09-724-108-21
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CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: US 09/009,388
PRIOR FILING DATE: 1998-01-20
                                                                                                                   301 GGCACCAAGCTGGAGCTCAAA 321
                                                                                           301 GGGACCAAGCTGGAGCTGAAA 321
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SOFTWARE: Patentin version 3.0
SEQ ID NO 21
LENGTH: 366
TYPE: DNA
ORGANISM: artificial sequence
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US-09-724-108-22
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NAME: Benjamin Aaron Adler, Ph.D.
REGISTRATION NUMBER: 35,423
| REFERENCE/DOCKET NUMBER: D661
| TELECOMMUNICATION INFORMATION:
| TELEPAN: (713) 777-2321
| TELEPAN: (713) 777-2321
| TELEPAN: (713) 777-6908
| INFORMATION FOR SEQ ID NO: 21:
| SEQUENCE CHARACTERISTICS:
| LENGTH: 366 bp
| TYPE: nucleic acid STRANDEDNESS: double-stranded
| TYPE: nucleic acid STRANDEDNESS: double-stranded
| TOPOLOGY: linear NOLECULE TYPE: nucleic acid HYPOTHETICAL: no
| HYPOTHETICAL: no
| HYPOTHETICAL: no
| SANTI-SENSE: no
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Sequence 18, Appli Sequence 8, Appli Sequence 13, Appli Sequence 13, Appl Sequence 13, Appl

Sequence 3, Sequence 3,

Sequence 62, Appl Sequence 62, Appl Sequence 18, Appl Sequence 8, Appli

Sequence

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Run on:

Sequence:

Searched:

Database

Result

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APPLICANT: Wong, Hing C.
Jiao, Jin-an
Esperanza, Nieves
Lawrence.
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSE: Dike, Bronstein, Roberts & Cushman, LLP STREET: 130 Water Street
CITY: Boston
STATE: MA
COUNTRY: USA
US-10-239-656-7
US-09-791-551-51
US-10-153-852-18
US-10-612-497-62
US-10-776-649-62
US-10-085-368-18
US-09-897-51A-8
US-09-897-51A-8
US-10-397-59-8
US-10-37-7079-8
US-10-37-7079-8
US-10-37-7079-8
US-10-947-811-8
US-10-947-811-3
US-10-347-81-3
US-10-347-81-13
US-10-37-81-13
US-10-759-115-13
US-10-759-115-13
US-10-759-13-13-13
US-10-94-881-8
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US-10-289-181-3
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FILING DATE: 16-Apr-1999
CLASSIFICATION: <UNKNOWN>
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APPLICATION NUMBER: 08/814,806
ATTORNEY/AGENT INFORMATION:
NAME: Corless, Peter F
REGISTRATION NUMBER: 33,860
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FRACES VERSION 1.5 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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  US-09-293-854-1
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Sequence 13, Appli
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Sequence 21, Appl
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Sequence 1, Appli
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1: /cgn2_6/ptodata/1/pubpna/USO1_PUBCOMB.seq:*

2: /cgn2_6/ptodata/1/pubpna/USO8_PUBCOMB.seq:*

3: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

4: /cgn2_6/ptodata/1/pubpna/USO9A_PUBCOMB.seq:*

5: /cgn2_6/ptodata/1/pubpna/USOAB_PUBCOMB.seq:*

6: /cgn2_6/ptodata/1/pubpna/USOAB_PUBCOMB.seq:*

7: /cgn2_6/ptodata/1/pubpna/USOD_PUBCOMB.seq:*

8: /cgn2_6/ptodata/1/pubpna/USOD_PUBCOMB.seq:*

9: /cgn2_6/ptodata/1/pubpna/USOD_PUBCOMB.seq:*

10: /cgn2_6/ptodata/1/pubpna/USOD_PUBCOMB.seq:*
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                       GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-09-990-586-1
US-10-293-417-1
US-10-310-113-1
US-10-230-880-1
US-10-764-140-1
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US-11-036-098-17
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US-10-073-644C-3
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                       - nucleic search, using sw model
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Gapop 10.0 , Gapext 1.0
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Maximum DB seq length: 200000000
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US-10-293-417-1
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Publication No. US20030109680A1
GENERAL INFORMATION:
APPLICANT: JIAO, JIN-AN
APPLICANT: JIAO, JIN-AN
TITLE OF INVENTION: OF USE THEREOF;
FILE REFRENCE: 71758/46543-CTP2
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT APPLICATION NUMBER: US/09/990,586
CURRENT APPLICATION NUMBER: 09/293,854
FRIOR FILING DATE: 1999-04-16
NUMBER OF SEQ ID NOS: 102
SOFTWARE: PARCHING PARCHING NOS: 102
SOFTWARE: PARCHING NOS: 102
SEQ ID NO 1
LENGTH: 321
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                                                                                                                               Query Match 100.0%; Score 321; DB 3; 1
Best Local Similarity 100.0%; Pred. No. 7e-94;
Matches 321; Conservative 0; Mismatches 0;
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Best Local Similarity 100.0%; Pred. No. 7e-94;
Matches 321; Conservative 0; Mismatches 0;
                                              ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-293-854-1
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              ANTI-SENSE: NO
PRAGMENT TYPE: <Unknown>
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; LOCATION: (1)..(321)
US-09-990-586-1
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                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1, Application US/10293417
Publication No. US20030082636A1
GENERAL INFORMATION:
APPLICANT: Woog, Hing C.
Jiao, Jin-an
Esperanza, Nieves
Lawrence, Luepschen
TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 5; Length 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: DISSUED COMPUTER: DISSUED COMPUTER: IEM COMPATIBLE COMPUTER: IEM COMPATIBLE COMPUTER: IEM COMPATIBLE COMPATIBLE CATTON DATA:

APPLICATION NUMBER: US/10/293,417
FILING DATE: 12-NO. US20030082636A1-2002
CLASSIFICATION DATA:
APPLICATION NUMBER: US/09/293,854
FILING DATE: 16-Apr-1999
APPLICATION NUMBER: 08/814,806
FILING DATE: CANANION:
ATTORNEY/AGENT INFORMATION:
NAME: COLIBES, POLE F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        100.0%; Score 321;
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 33,860
REFERENCE/DOCKET NUMBER: 46
                                                                                                                                                                                                                                     301 GGGACCAAGCTGGAGCTGAAA 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 617-523-6440
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Boston
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ANTI-SENSE: NO
FRAGMENT TYPE: <
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121 GGGAAATCTCCTCAGCTCCTGATTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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                                          AGGTTCAGTGGCAGTGGATCTGGCACAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
                                                                                                                  181 AGGITCAGIGGCAGIGGAICIGGCACAAAITITICITICAAGAICAGCAGCCIACAGGCI
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Sequence 1, Application US/10230880

Publication No. US20030190705A1

GENERAL INFORMATION:
APPLICANT: WONG, HING C.
TITLE OF INVENTION: METHOD OF HUMANIZING IMMUNE SYSTEM MOLECULES
FILE REPERBNCE: 71758/5806

CURRENT FILING DATE: 2002-12-23

PRIOR PILING DATE: 2001-11-21

PRIOR PLICATION NUMBER: 09/990,586

PRIOR PLING DATE: 2001-11-21

PRIOR PLING DATE: 2001-10-29

PRIOR FILING DATE: 1999-04-16

NUMBER OF SEQ ID NOS: 174

SEQ ID NO 1.
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ORGANISM: Homo sapiens
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; LOCATION: (1)..(321)
US-10-230-880-1
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                                                                                                                              61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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APPLICANT: JIAO, JIN-AN
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
APPLICANT: WONG, HING C.
TITLE OF INVENTION: USE DO ANTI-TISSUE FACTOR ANTIBODIES FOR TREATING
TITLE OF INVENTION: THROMBOSES
TITLE OF INVENTION: THROMBOSES
TITLE OF INVENTION: THROMBOSES
TITLE OF INVENTION: UNMBER: US/10/310,113
CURRENT FILING DATE: 2002-12-04
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: 60/343,306
PRIOR PLILING DATE: 2001-11-0.29
PRIOR APPLICATION NUMBER: 09/293,854
PRIOR APPLICATION NUMBER: 08/814,806
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1999-04-16
PRIOR FILING DATE: 1990-03-10
NUMBER OF SEQ ID NOS: 169
SOFTWARE: PALCETIN VET. 2.1
                                                                                                                                                                                                GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA
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                 Pred. No. 7e-94;
; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%; Pre-
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Best Local Similarity 100.0
Matches 321; Conservative
                                  321; Conservative
               Best Local Similarity
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LOCATION: (1)
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LENGTH: 321
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Sequence 1. Application US/10764140

Publication No. US20040229282A1

Publication No. US20040229282A1

GENERAL INFORMATION:

APPLICANT: WONG, HING C.

APPLICANT: WONG, HING C.

TITLE OF INVENTION: OF USE THEREOF

CURRENT APPLICATION NUMBER: US/10/764,140

CURRENT APPLICATION NUMBER: 10/293,417

PRIOR FILING DATE: 2002-11-12

PRIOR FILING DATE: 2002-04-16

PRIOR FILING DATE: 2002-04-16

PRIOR FILING DATE: 2002-04-16

PRIOR FILING DATE: 2002-03-10

NUMBER OF SEQ ID NOS: 26

SOFTWARE: Patentin Ver. 3.2

SEQ ID NO 1

LENGTH: 321
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Lawrence, Luepschen
TITLE OF INVENTION: ANTHONOUSE FOR INHIBITING BLOOD
COAGULATION AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match 100.0%; Score 321; DB 8; Length 321; Best Local Similarity 100.0%; Pred. No. 7e-94; Matches 321; Conservative 0; Mismatches 0; Indels
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Dike, Bronstein, Roberts & Cushman, LLP
STREET: 130 Water Street
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Publication No. US20050089929A1
GENERAL INFORMATION:
APPLICANT: Wong, Hing C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Mus musculus
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100.0%; Score 321; DB 9; Length 3
Best Local Similarity 100.0%; Pred. No. 7e-94;
Matches 321; Conservative 0; Mismatches 0; Indels
                                                                                                                                                                    COMPUTER: IDENCE COMPUTER: IDENTE COMPUT
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MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANII-SENSE: NO
FRACHENT TYPE: <Unknown>
ORIGINAL SOURCE:
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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US-10-462-062-12
'Sequence 12, Application US/10462062
'Publication No. US/0040044187Al
'GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 321 base pairs
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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STRANDEDNESS: singl
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RESULT 10
US-11-036-098-15
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LOCATION: (1)..(375)
FRATURE:
NAME/KEY: sig_peptide
LOCATION: (1)..(54)
FEATURE:
LOCATION: (1)..(54)
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TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
TITLE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMANIZED ANTIBODIES
TITLE OF INVENTION: HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0360
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT FILING DATE: 1090-04-02
PRIOR FILING DATE: 1999-04-03
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: PATCHIN Ver. 2.1
LENGTH 375
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Publication No. US20040044187A1
GENERAL INFORMATION:
APPLICANT: SATO, KOH
APPLICANT: ADACHI, HIDEKI
ITILE OF INVENTION: HUMANIZED ANTIBODIES AGAINST HUMAN TISSUE FACTOR (TF)
ITILE OF INVENTION: AND PROCESS OF PRODUCTION OF THE HUMANIZED ANTIBODIES
FILE REFERENCE: 053466-0108
CURRENT APPLICATION NUMBER: US/10/462,062
CURRENT PILING DATE: 2003-06-16
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                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
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Best Local Similarity 94.74
Matches 304; Conservative
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; LOCATION: (55)..(375)
US-10-462-062-12
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Sequence 15, Application US/11036098
| Publication No. US20050163770A1
| GENERAL INFORMATION:
| APPLICANT: Connex GmbH
| TITLE OF INVENTION: Extracellular domain of the human zeta chain
| TITLE OF INVENTION: Extracellular domain of the human zeta chain
| TITLE OF INVENTION: Extracellular domain of the human zeta chain
| TITLE OF INVENTION: Extracellular domain of the human zeta chain
| FILE REFERENCE: C1368PCT |
| CURRENT PEDLICATION NUMBER: US/11/036,098 |
| FRICH RAPPLICATION NUMBER: US/09/743,482 |
| PRIOR FILING DATE: 2001-02-28 |
| PRIOR FILING DATE: 2001-02-28 |
| PRIOR FILING DATE: 1998-07-10 |
| NUMBER OF SEQ ID NOS: 18 |
| SEQ ID NO 15 |
| LENGTHE: Patentin Ver. 2.1 |
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: Description of Artificial Sequence: Nucleotide sequence OTHER INFORMATION: coding for L chain V region of anti-TF mouse monoclonal PEATURE:
NAME: NAM
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PRIOR APPLICATION NUMBER: PCT/JP99/01768
PRIOR FILING DATE: 1999-04-02
PRIOR APPLICATION NUMBER: JP 10-91850
PRIOR FILING DATE: 1998-04-03
NUMBER OF SEQ ID NOS: 183
SOFTWARE: Patentin Ver. 2.1
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; LOCATION: (55)..(375)
US-10-462-062-13
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1 GACGICCIGGIGACCCAAACICCIGCCICCCIGICAGCATCIGCATCAGCC
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Best Local Similarity 84.1
Matches 270; Conservative
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Publication No. US20040146976A1

GENERAL INFORMATION:
GENERAL INFORMATION:
GENERAL INFORMATION:
TITLE OF INVESTION:
TITLE OF INVESTION:
FILE SEFERENCE: 97-99E

CURRENT FLING DATE: 2003-12-16

PRIOR APPLICATION NUMBER: US 99/724,108

PRIOR APPLICATION NUMBER: US 09/724,108

PRIOR APPLICATION NUMBER: US 09/009,388

PRIOR PRILING DATE: 1999-01-20

PRIOR PRILING DATE: 1998-01-20

PRIOR APPLICATION NUMBER: US 60/018,741

PRIOR PLILING DATE: 1997-05-30

PRIOR APPLICATION NUMBER: US 60/018,741

NUMBER OF SEQ ID NOS: 26

SOFTWARE: PARCENT PARCENT
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                                                                                                                                                                                DB 10; Length 321;
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                                                                                                                                                                             Score 239.4; DB Pred. No. 2.7e-67 0; Mismatches 5:
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Best Local Similarity 84.1%;
Matches 270; Conservative (
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ORGANISM: artificial sequence
                     ) OKGANISM: Rattus norvegicus
; FRATURE:
NAMB/KEY: CDS
; LOCATION: (1)..(321)
US-11-036-098-15
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US-10-738-454-21
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WESULO 12

9 Sequence 22, Application US/10738454

9 Publication No. US20040146976A1

1 GENERAL INFORMATION:

1 APPLICANT: The Board of Trustees of the University of Illinois

1 APPLICANT: Wittrup, et al.

1 TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof

1 TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof

1 TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof

1 FILE REFERENCE: 97-99E

1 CURRENT APPLICATION NUMBER: US 09/724,108

1 PRIOR FILING DATE: 2000-11-28

1 PRIOR FILING DATE: 1998-01-20

2 PRIOR FILING DATE: 1997-05-30

2 PRIOR FILING DATE: 1997-05-30

3 PRIOR FILING DATE: 1997-05-30

3 PRIOR FILING DATE: 1997-05-31

3 NUMBER OF SEQ ID NOS: 26

3 SOFTWARE: Patentin version 3.0

5 SEQ ID NO 22

1 LENGTH: 366
                                                                                                                                                                                      180
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61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA
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                                                                                                                                                                                                                                                                                                                  181 AGGTTCAGTGGCAGTAGATCTGGCACACAGTATTCTCTTAAGATCAACAGACTACAGGTT
                                                                                                                            GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA
                                                                                                                                                                                                                                                                                                                                                                                         GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT
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Pred. No. 2.9e-67;
0; Mismatches 51.
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US-10-738-454-22
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Sequence 17, Application US/1103698
| Publication No. US20050163770A1
| GENERAL INFORMATION:
| APPLICANT: Connex GmbH
| TITLE OF INVENTION: Extracellular domain of the human zeta chain
| FILE REFERENCE: C1368PCT.
| FILE REFERENCE: C1368PCT.
| CURRENT APPLICATION NUMBER: US/11/036,098
| CURRENT FILING DATE: 2005-01-18
| PRIOR PRILICATION NUMBER: US/09/743,482
| PRIOR FILING DATE: 2001-02-28
| PRIOR FILING DATE: 1998-07-10
| PRIOR FILING DATE: 2001-02-28
| PRIOR PRILICATION NUMBER: EP 98 11 2867.1
| PRIOR FILING DATE: 2001-02-28
| PRIOR FILING DATE: 2001-02-28
| PRIOR PRILICATION NUMBER: EP 98 11 2867.1
| PRIOR PRILICATION NUMBER: EP 98 11 2867.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; OTHER INFORMATION: PCR products of KJ16-mut7
US-10-738-454-23
CURRENT FILING DATE: 2003-12-16
PRIOR APPLICATION NUMBER: US 09/724,108
PRIOR FILING DATE: 2000-11-28
PRIOR PILING DATE: 1998-01-20
PRIOR FILING DATE: 1998-01-20
PRIOR PILING DATE: 1997-05-30
PRIOR PILING DATE: 1997-05-30
PRIOR FILING DATE: 1997-05-31
NUMBER OF SEQ ID NOS: 26
SOUTHARE: PatentIn version 3.0
SEQ ID NO 23
LENGTH: 366
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ORGANISM: artificial sequence
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ORGANISM: Artificial Sequence
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US-11-036-098-17
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                                                        Sequence 23, Application US/10738454
Publication No. US20040146976A1
GENERAL INFORMATION:
APPLICANT: The Board of Trustees of the University of Illinois
APPLICANT: Witrup, et al.
TITLE OF INVENTION: Yeast Cell Surface Display of Proteins and Uses Thereof
FILE REFERENCE: 97-99E
CURRENT APPLICATION NUMBER: US/10/738,454
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TITLE OF INVENTION: Detection of Patients at Risk for Developing Integrin
TITLE OF INVENTION: Antegoniat/Agonist Mediated Disease States
TITLE OF INVENTION: Antegoniat/Agonist Mediated Disease States
CURRENT APPLICATION NUMBER: US/09/237,061
CURRENT FILING DATE: 1999-01-26
PRIOR APPLICATION NUMBER: 60/072,733
NUMBER OF SEQ ID NOS: 2.0
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                            GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ) OTHER INFORMATION: Description of Artificial Sequence: Light Chain of COTHER INFORMATION: rJK094
US-09-237-061-1
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                                                                                                                              301 GGGACCAAGCTGGAGCTGAAA 321
                                                                                                                                                                301 GGGACCAAGCTGGAGCTGAAA 321
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                                                                                                                                                                                                                                                                                                                        Sequence 1, Application US/09237061
Patent No. US20020081624A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ORGANISM: Artificial Sequence
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LENGTH: 724
                            241
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                                                                                                                                       61 ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
                                                                                                                                                                                1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAGTGTCACC 60
                                                                          Gaps
; OTHER INFORMATION: construct of DNA encoding bispecific single chain oTHER INFORMATION: antibody comprising anti-zeta-chain/anti-EpCAM content information: domains.
                                                  Score 236.2; DB 10; Length 1637;
Pred. No. 5.9e-66;
0; Mismatches 53; Indels 0;
                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity 83.5%;
Matches 268; Conservative
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Search completed: April 18, 2006, 22:26:16 Job time : 575 secs

Sequence:

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Run

Searched:

Database

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Sequence 1, Application US/11122622
| Publication No. US20060039901A1
| GENERAL INFORMATION:
| APPLICANT: JIAO, JIN-AN
| APPLICANT: WONG, HING C.
| TITLE OF INVENTION: ANTIBODIES FOR INHIBITING BLOOD COAGULATION AND METHODS
| TITLE OF INVENTION: OF USE THEREOF
| FILE REFERENCE: 71758/46943-CIP2
| CURRENT FALLING DATE: 2005-05-05
| FRIOR FILING DATE: 2005-05-05
| FRIOR FILING DATE: 2001-11-21
| FRIOR FILING DATE: 1999-04-16
| NUMBER OF SEQ ID NOS: 102
| SOFTWARE: PATENTING DATE: 2001-11-16
| SOFTWARE: PATENTING DATE: 1999-04-16
| NUMBER OF SEQ ID NOS: 102
| SEQ ID NO 1
| SEQ ID NO 1
                           Sequence 187, A Sequence 51, Ap Sequence 51, Ap Sequence 59, Sequence 453, Sequence 121, A Sequence 121, A Sequence 13, A Sequence 206, A Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GACATTCAGATGACCCAGTCTCCTCCCTCCCAGTCTGCATCTCTGGGAGAAAAGTGTCACC
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4 US-11-182-343-53

US-10-893-483-187

US-10-893-483-187

4 US-11-155-775-51

4 US-11-136-250-5

1 US-11-199-739-597

4 US-11-199-739-597

4 US-11-199-739-597

US-11-049-536-453

US-11-049-536-453

US-11-049-536-413

US-11-05-453-75-55

US-11-144-222-13

US-11-144-222-13

US-11-144-222-13

US-11-10-139-739-481

US-11-049-536-481

US-11-009-840A-206

US-11-009-840A-206

US-11-009-84-81

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US-11-009-84-81

US-11-009-81-81

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Pred. No. 2.4e-92;
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100.0%; Score 321; D
Best Local Similarity 100.0%; Pred. No. 2.4
Matches 321; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LOCATION: (1) .. (321)
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Best Local Similarity
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       US-11-122-622-1
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Sequence 190, App
Sequence 426, App
Sequence 188, App
Sequence 54, Appl
Sequence 54, Appl
Sequence 7, Appl
Sequence 17, Appl
Sequence 173, App
Sequence 173, App
Sequence 75, Appl
Sequence 75, Appl
Sequence 241, App
Sequence 241, App
Sequence 541, App
Sequence 541, App
Sequence 531, Appl
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                                                                                                                                                           April 18, 2006, 18:31:21; Search time 1340 Seconds (without alignments) 964.876 Million cell updates/sec
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                                                                                                                                                                                                                                                                                                            1 gacattcagatgacccagtc......ggaccaagctggagctgaaa 321
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1: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
2: /SIDS5/ptodata/2/pubpna/US08_NEW_PUB.seq:*
3: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
4: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
5: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
6: /SIDS5/ptodata/2/pubpna/US07_NEW_PUB.seq:*
7: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
8: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
9: /SIDS5/ptodata/2/pubpna/US10_NEW_PUB.seq:*
11: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
12: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
13: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
14: /SIDS5/ptodata/2/pubpna/US11_NEW_PUB.seq:*
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17: /SIDS5/ptodata/2/pubpna/US01_NEW_PUB.seq:*
18: /SIDS5/ptodata/2/pubpna/US01_NEW_PUB.seq:*
                           GenCore version 5.1.7
Copyright (c) 1993 - 2006 Biocceleration Ltd
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US-11-087-528-1

US-11-136-527-190

US-11-136-527-190

US-11-128-900-62

US-11-144-248-54

US-11-144-222-54

US-11-144-222-54

US-11-080-33-188

US-11-080-33-188

US-11-199-73-173

US-11-199-739-173

US-11-199-739-173

US-11-199-739-241

US-11-199-739-241

US-11-199-739-241

US-11-199-739-241

US-11-199-739-241

US-11-144-248-53
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Maximum Match 100%
Listing first 45 summaries
                                                                                                                   OM nucleic - nucleic search, using sw model
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Maximum DB seq length: 200000000
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Match ]
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Sequence 21,

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Result No.

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RESULT 4
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Publication No. US20050271664A1

Sequence 1, Application US/11087528

Publication No. US20050271664A1

GAPERALL INFORMATION:

APPLICANT: WONG, HING C.

PRIOR PELING DATE: 1099-04-16

PRIOR APPLICANT: NUMBER: 09/293, 854

PRIOR APPLICANT: NUMBER: 09/293, 854

PRIOR APPLICANT: 1997-03-10

NUMBER: OF SEQ ID NOS: 26

SOFTWARE: PARCENT: 1997-03-10

SEQ ID NO: 26

SEQ ID NO: 27

APPLICANT: WONG, MONG, 
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121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                        181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT 240
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                                                                                                181 AGGITCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
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Pred. No. 2.4e-92;
0; Mismatches 0;
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Best Local Similarity 100.0%;
Matches 321; Conservative 0
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LOCATION: (1)..(321)
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85 GACATCCATGTGACACACAGTCTCCTGCCTCCCTGTCTGCATCTCCGGAAGAAATTRTCACC 144
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Sequence 4286, Application US/11136527

Publication No. US20050287570A1

GENERAL INFORMATION:

APPLICANT: Wyeth

APPLICANT: Wounts, William M

TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes

FILE REFERENCE: 031896-041000 (ANIO1086)

CURRENT FILING DATE: 2005-05-25

PRIOR APPLICATION NUMBER: US 60/574,294

PRIOR PAPLICATION NUMBER: US 60/574,294

PRIOR PLING DATE: 2005-05-26

NUMBER OF SEQ ID NOS: 362830

SOFTWARE: Patentin version 3.2

SEQ ID NO 4286

LENGTH: 411
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                                                                              APPLICANT: Wyeth
APPLICANT: Wounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
APPLICANT: Mounts, William M
TITLE OF INVENTION: Probe Arrays For Expression Profiling of Rat Genes
FILE REFERENCE: 031895-041000 (AM101086)
CURRENT APPLICATION NUMBER: US/11/136,527
PRIOR APPLICATION NUMBER: US 60/574,294
PRIOR FILING DATE: 2005-05-26
NUMBER OF SEQ ID NOS: 362830
SOFTWARE: Patentin version 3.2
SET IN O 199
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Sequence 190, Application US/11136527
Publication No. US20050287570A1
GENERAL INFORMATION:
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Best Local Similarity 82.2*
Matches 264; Conservative
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    GAAGATTTTGTAAATTAATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
                                                                 AGGITCAGIGGCAGIGGAICIGGCACAAAAITITCITICAAGAICAGCAGCCIACAGGCI
                                                                                          307 GAAGATTTTGCAACTTACTACTGTCAACAGTATTACAGTACTCCATTCACTTTCGGCCCT
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                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Buelow, Roland
APPLICANT: Blatzer, Josef
APPLICANT: Blatzer, Josef
APPLICANT: Schooten, Wim van
TITLE OF INVENTION: Humanized Immunoglobulin Loci
FILE REFERENCE: 35591-0007A
CURRENT APPLICATION UWBER: US/10/893,483
CURRENT PILING DATE: 2004-07-15
PRIOR APPLICATION NUMBER: 60/487,733
PRIOR FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FASTSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; OTHER INFORMATION: Humanized light chain locus US-10-893-483-188
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                                                                                                                                                                                                                         GGGACCAAGCTGGAGCTGAAA 321
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Publication No. US20050244408A1
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ORGANISM: Artificial Sequence
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LENGTH: 13281
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APPLICANT: HANSON, DOUGLAS C.

APPLICANT: NEVEN.

APPLICANT: MUSILER, BILEEN E.

APPLICANT: MUSILER, BILEEN E.

APPLICANT: GILANN, STEVEN C.

APPLICANT: GLANN, STEVEN C.

APPLICANT: CORVALAN, JOSE N.

TITLE OF INVENTION: HUMAN MONOCLONAL ANTIBODIES TO CTLA-4

FILE REFERENCE: ABX-PF1 DIV3

CURRENT APPLICATION NUMBER: US/11/128,900

CURRENT FILING DATE: 2005-05-12

PRIOR APPLICATION NUMBER: US 10/76649

PRIOR APPLICATION NUMBER: US 09/472087

PRIOR APPLICATION NUMBER: US 09/472087

PRIOR APPLICATION NUMBER: US 09/472087

PRIOR PILING DATE: 1999-12-23

PRIOR FILING DATE: 1999-12-23

NUMBER OF SEQ ID NOS: 147

SOFTWARE: PATENTIN VET.

LENGTH: 714
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                      Indels
    ed. No. 1.9e-66;
Mismatches 36;
82.2%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GGGACCAAGCTGGAGCTGAAA 321
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; Publication No. US20050287136A1
; GENERAL INFORMATION:
                    264; Conservative
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ORGANISM: Homo sapiens
Best Local Similarity
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US-11-128-900-62
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ; OTHER INFORMATION; Description of Artificial Sequence: Consensus Sequence US-11-182-343-54
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                                                                                                                                                                                                  ) OTHER INFORMATION: Description of Artificial Sequence: Consensus; OTHER INFORMATION: sequence
US-11-144-222-54
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                                                                                                                                                                                                                                                                                                     DB 14; Length 322;
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70.0%; Score 224.6; DB 14; Length 322;
Best Local Similarity 78.5%; Pred. No. 1.7e-61;
Matches 252; Conservative 12; Mismatches 57; Indels 0;
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APPLICANT: Gualberto, Antonio
APPLICANT: Gualberto, Antonio
APPLICANT: Gualberto, Antonio
APPLICANT: Melvin, Carrie
APPLICANT: Melvin, Carrie
APPLICANT: Reberts, Luisa M.
TITLE OF INVENTION: COMBINATION TREATMENT FOR BREAST CANCER
FILE REFERENCE: PG2226A
CURRENT APPLICATION NUMBER: 2005-07-15
PRIOR APPLICATION NUMBER: 60/588,721
PRIOR FILING DATE: 2004-07-16
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin version 3.3
SEQ ID NO 54
LENGTH: 322
                                                                                                                                                                                                                                                                                                   Query Match 70.0%; Score 224.6; DB 14; Length Best Local Similarity 78.5%; Pred. No. 1.7e-61; Matches 252; Conservative 12; Mismatches 57; Indels
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; Publication No. US20060018910A1
; GENERAL INFORMATION:
                                                                                                                               TYPE: DNA ORGANISM: Artificial Sequence
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PRIOR FILING DATE: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 54
LENGTH: 322
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                      APPLICANT: Cohen, Bruce D.
APPLICANT: Cohen, Miler, Penelope E.
APPLICANT: Miler, Penelope E.
APPLICANT: Miler, Penelope E.
APPLICANT: Moyer, James D.
APPLICANT: Gorvalan, Jose R.
APPLICANT: Gallo, Michael
ITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE OF INVENTION: ANTIBODIES TO SOUTH FACTOR I RECEPTOR FILE REFERENCE: ABX-PF2
CURRENT APPLICATION NUMBER: US/10/038,591
PRIOR PILING DATE: 2002-01-04
PRIOR PAPLICATION NUMBER: 60/259,927
PRIOR APPLICATION UMBER: 60/259,927
PRIOR APPLICATION UMBER: 60/259,927
PRIOR APPLICATION UMBER: 2001-01-05
NUMBER OF SEQ ID NOS: 60
SOFTWARE: Patentin Ver. 2.1
LENGTH: 322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 ATCACTTGCCGGCAAGTCAGAGCATTAGYASCTWTTTAAATTGGTATCAGCAGAAACCA 120
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Publication No. US20050281812A1
Sequence 54, Application US/11144222
Publication No. US20050281812A1
SERREAL INFORMATION:
APPLICANT: Gohen, Bruce D.
APPLICANT: Miller, Penelope E.
APPLICANT: Miller, Penelope E.
APPLICANT: Gordan, Jose R.
APPLICANT: Gallo, Michael
TITLE OF INVENTION: ANTIBODIES TO INSULIN-LIKE GROWTH FACTOR I RECEPTOR FILE NEFERENCE: ABX-PPS
CURRENT APPLICATION NUMBER: US/11/144,222
CURRENT FILING DATE: 2005-06-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OTHER INFORMATION: Description of Artificial Sequence: Consensus; OTHER INFORMATION: sequence
US-11-144-248-54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 12; Length 322;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US/10/038,591
PRIOR FILING DATE: 2002-01-04
PRIOR APPLICATION NUMBER: 60/259,927
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US-11-144-222-54
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Gaps

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; Sequence 188, Application US/10893483
; Publication No. US20060026696A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                TYPE: DNA
ORGANISM: Artificial Sequence
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                   GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                                                                                                                                          240
                                                                                                                                                                                                           GAAGATTTTGTAAATTATTACTGTCAACAAGTTTACAGTTCTCCATTCACGTTCGGTGCT 300
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                                                                                                                                      AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGCT
                                                                                                                                                          1 GACATTCAGATGACCCAGTCTCCTGCCTCCCAGTCTGCATCTCTGGGAGAAAGTGTCACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      247 AGGITCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGTCTGCAACCT
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Pred. No. 1.9e-60;
0; Mismatches 62; Indels
                                                                                                                                                                                                                                                                                                                                                                                           SQUENCE OF APPLICATION US/11086289
| Publication No. US200600029291
| GENERAL INFORMATION:
| GENERAL INFORMATION:
| APPLICANT: KHALE SANJAY D. |
| APPLICANT: KELLERMANN, SIRID-AIMEE ITILE OF INVENTION: MONOCLONAL ANTIBODIES FILE REFERENCE: 06843.0094-00000 |
| CURRENT APPLICATION NUMBER: US/11/086,289 |
| CURRENT FILING DATE: 2005-03-23 |
| PRIOR FILING DATE: 2004-03-23 |
| NUMBER OF SEQ ID NOS: 26 |
| SOFTWARE: PATENTIN OFF. 2004-03-23 |
| SENGTHARE: PATENTIN OFF. 3.3 |
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Matches 259; Conservative
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RESULT 11

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121 GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62; Indels
APPLICANT: Buelow, Roland
APPLICANT: Blatzer, Josef
APPLICANT: Blatzer, Josef
APPLICANT: Schooten, Wim van
TITLE OF INVENTION: Humanized Immunoglobulin Loci
FILE REFERENCE: 39691-0007A
CURRENT APPLICATION NUMBER: US/10/893,483
CURRENT FILING DATE: 2004-07-15
FRIOR FILING DATE: 2003-07-15
NUMBER OF SEQ ID NOS: 460
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 188
LENGTH: 13281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             US-11-199-173
US-11-199-173
Sequence 173, Application US/11199739
Sequence 173, Application US/11199739
GENERAL INFORMATION:
APPLICANT: Wood, Clive R.
APPLICANT: Pieters, Henk
APPLICANT: Pieters, Henk
APPLICANT: Pieters, Henk
APPLICANT: Pieters, Henk
APPLICANT: Pieters, US-11, 199, 739
CURRENT FILTON TE COMPLEX BINDING PROTEINS
FILE REFERENCE: 10280-135001
CURRENT APPLICATION NUMBER: US/11/199, 739
CURRENT APPLICATION NUMBER: US 11/049,536
PRIOR FILLING DATE: 2005-02-02
PRIOR PELICATION NUMBER: US 10/916,840
PRIOR FILLING DATE: 2004-08-12
PRIOR FILLING DATE: 2004-08-12
PRIOR FILLING DATE: 2004-08-12
PRIOR FILLING DATE: 2003-08-12
NUMBER OF SEQ ID NOS: 726
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match 69.1%; Score 221.8; DB 9; Best Local Similarity 80.7%; Pred. No. 7.3e-60; Matches 259; Conservative 0; Mismatches 62;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Humanized light chain locus
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ATCACATGCCTGGCAAGTCAGACCATTGATACATGGTTAGCATGGTATCAGCAGAAACCA 120
                                                                                                                                                    GGGAAATCTCCTCAGCTCCTGATTTATGCTGCCACCAACTTGGCAGATGGGGTCCCATCA 180
                                                                                                                                                                                       181 AGGTTCAGTGGCAGTGGATCTGGCACAAAATTTTCTTTCAAGATCAGCAGCCTACAGGGCT 240
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                                                                184 AGGTTCAGTGGCAGTGGATCTGGGACAGATTTCACTCTCACCATCAGCAGCTGCAACCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               121 GGGAAAGCCCCTAAGCTCCTGATGCTGCATCCATTTTACAAAGTGGGGTCCCATCA
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Sequence 75, Application US/10956008

Publication No. US20060062783A1

GENERAL INFORMATION:

APPLICANT: Foltz, Ian

APPLICANT: King, Chadwick

APPLICANT: King, Chadwick

APPLICANT: ANTIBODIES

PILE REFERENCE: ABGENIX.092CP1

CURRENT FILING DATE: 2004-09-30

PRIOR APPLICATION NUMBER: 10/638,265

PRIOR FILING DATE: 2003-08-08

NUMBER OF SEQ ID NOS: 110

SOFTWARE: FastSEQ for Windows Version 4.0

SED ID NO 75

SEQ ID NO 75
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Pred. No. 1.4e-59;
0; Mismatches 64
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Best Local Similarity 80.1%;
Matches 257; Conservative (
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; ORGANISM: Homo sapiens
US-10-956-008-75
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                                                                                                                                                                                                                                                                              Score 220.2; DB 11; Length 324;
Pred. No. 4.3e-60;
0; Mismatches 63; Indels 0;
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Pred. No. 4.3e-60;
0; Mismatches 63; Indels
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; Sequence 173, Application US/11049536
; Publication No. US20060024297A1
; GENERAL INFORMATION:
; APPLICANT: Wood, Clive R.; APPLICANT: Wood, Clive R.; APPLICANT: Pieters, Henk
; APPLICANT: Pieters, Henk
; APPLICANT: Hufton, Simon E.; TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
; FILE REFERENCE: 10280-128001
; CURRENT APPLICATION NUMBER: US/11/049,536
; CURRENT PILING DATE: 2005-02-02
; PRIOR FILING DATE: 2005-02-02
; PRIOR FILING DATE: 2003-08-12
; NUMBER OF SEQ ID NOS: 721
; SOFTWARE: FRASESQ for Windows Version 4.0
; SEQ ID NO 173
SOFTWARE: FastSEQ for Windows Version 4.0
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Matches 258; Conservative (
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Best Local Similarity 80.4%;
Matches 258; Conservative
                                                                                                                                                                                 ; OTHER INFORMATION: Antibody US-11-199-739-173
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US-11-049-536-173
                                                                                          TYPE: DNA ORGANISM: ARTIFICIAL
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US-11-049-536-173
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Sequence 241, Application US/11199739
Publication No. US20060057138A1
GENERAL INFORMATION:
APPLICANT: Wood. Clive R.
APPLICANT: Dransfield, Daniel T.
APPLICANT: Pieters, Henk
APPLICANT: Hofton, Simon E.
TITLE OF INVENTION: TIE COMPLEX BINDING PROTEINS
FILE REFRENCE: 10280-135001
CURRENT APLICATION NUMBER: US/11/199,739
CURRENT FILING DATE: 2005-08-09
PRIOR APPLICATION NUMBER: US 11/049,536
PRIOR APPLICATION NUMBER: US 10/916,840
PRIOR APPLICATION NUMBER: US 004-08-12
PRIOR APPLICATION NUMBER: US 004-94,713
PRIOR FILING DATE: 2004-08-12
NUMBER OF SEQ ID NOS: 726
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 241
LENGTH: 324
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; OTHER INFORMATION: Antibody US-11-199-739-241
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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EMBL; BC018455; AAH18455.1; -; mRNA.
HSSP; P01810; ZEBJ.
SWR; QOSVCV5; 2-0-239.
Ensembl; ENSWUSGO000021155; Mus musculus.
GO; GO:0003823; F:antigen binding; IEA.
InterPro; IPR00310; Ig-11ke.
InterPro; IPR003597; Ig-21.
InterPro; IPR003596; Ig-WC.
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NIH MGC Project;
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Last annotation update)
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07TQM2_MOUSE

06P34R8 MOUSE

HV07_MGUSE

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AC 01-WAR-2002 (TrEMBLrel. 20, DT 01-WAR-2002 (TrEMBLrel. 20, DT 01-WAR-2002 (TrEMBLrel. 20, DT 01-WAR-2004 (TrEMBLrel. 26, DE 10C238447) protein.

GN MAR-2004 (TrEMBLrel. 26, DE 10C238447) protein.

GN MAR-2004 (TrEMBLrel. 26, DE 10C238447) protein.

GN MAR-2004 (TrEMBLrel. 26, DT 02C38447) protein.

GN MAR-2004 (TrEMBLrel. 26, DT 02C38447) protein.

GN MAR-2004 (TrEMBLrel. 26, DT 02C38447) protein.

NUCLEOTIDE SEQUENCE.

RA Altachul S.F., Zeeberg B., I RA Strausberg R.L., Feingold E., I RA Altachul S.F., Zeeberg B., I RA Stapleton M., Soares M.B., RA Boack S.A., McEwan P.J., McI RA Stapleton D.K., Matan A., Young RA Blakesley R.W., Touchman J. RA Fahey J., Helton E., Kettem Whiting M., Madan A., Young RA Blakesley R.W., Touchman J. RA Generation and initial ana RT Generation and initial ana And mouse cDNA sequences., I R. NUCLEOTIDE SEQUENCE.

RY GENERALION SEQUENCE.

RY HWGC Project;

RY HKSP; PO1810; ZFBJ.

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BY HSSP; PO1810; ZFBJ.

BY HTEFFPO; IPRO03597; IQ-C1.

BY INTEFFPO; IPRO03597; IQ-C1.

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HV14 MOUSE

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HV15_MOUSE

HV15_MOUSE

058E56_MOUSE

058E56_MOUSE
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Q65ZR6 MOUSE
Q4VAB6 MOUSE
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Maximum Match 100%
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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.MEDLINE-92281444; PubMed=1512540; DOI=10.1084/jem.176.3.761;
Tillman D.M., Jou N.T., Hill R.J., Marion T.N.;
"Both IgM and IgG anti-1DNA antibodies are the products of clonally selective B cell stimulation in (NZB x NZW)FI mice.";
J. Exp. Med. 176.761-779(1992).
EMBL; AJZ25511; CAB65236.1; -; mRNA.
PIR; PH0973; PH0973.
                                                                                                                                                                                         Length 481;
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, Clemens A., Rademaekers A., Specht C., Koelsch E.; Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                  Immunoglobulin domain.
SEQUENCE 481 AA; 52326 MW; 52B44C5826807143 CRC64;
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01-MAY-2000 (TYEMBLrel. 13, Last sequence update)
01-MAY-2004 (TYEMBLrel. 26, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
Mus musculus (Mouse).
                                                                                                                                                                                   Query Match 77.2%; Score 476.5; DB 2; Best Local Similarity 75.4%; Pred. No. 4.1e-39; Matches 89; Conservative 13; Mismatches 15;
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77.0%; Score 475; DB 2;
Best Local Similarity 76.1%; Pred. No. 1.2e-39;
Matches 89; Conservative 13; Mismatches 15;
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                   SMART; SM00406; IGV; 1.
PROSITE; PS50835; IG LIKE; 4.
PROSITE; PS00290; IG_MHC; UNKNOWN_2.
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InterPro, IPR003596; Ig-v.
SMART; SM00406; IGv; 1.
PR051TE; PS50835; IG_LIKE; 1.
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Q9QXF0;
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Q9QXE9;
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MUCLEOTIDE SEQUENCE.

MICLIME-91237115; PubMed=1709665;

MEDLINE-91237115; PubMed=1709665;

MILLIME-91237115; PubMed=1709665;

MILLIME-91237115; PubMed=1709665;

MILLIME-9124010; MILLIME THE COEXPICEBRION OF TWO MILLIME THEORY. PRO07110; 19-11ke.

MILLE-PRO. 1 PR003199; 19-1.

MILLE-PRO. 1 PR003199; 19-1.
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muridae, Murinae, Mus.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
NCBI_TaxID=10090;
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"Two murine natural polyreactive autoantibodies are encoded by nonmutated germ-line genes.";
Proc. Natl. Acad. Sci. U.S.A. 86.4624-4628 (1989).
EMBL, AJ225174; CAB65237.1; -; mRNA.
EMBL, AJ225174; CAB65237.1; -; mRNA.
EMS., PO1751; 1NQB.
SMR; Q9QXE9; 1-117.
InterPro; IPR001110; Ig-like.
InterPro; IPR001596; Ig_v.
SMART; SM0046; Ig_v.
SMART; SM0046; Ig_LKE; 1.
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25-OCT-2004 (TrEMBLrel. 28, Last sequence update)
25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
Ab 126.33 heavy chain variable and joining regions (Fragment).
Mus musculus (Mouse)
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Submitted (DEC-1997) to the EMBL/GenBank/DDBJ databases.
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01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Immunoglobulin heavy chain V-D-J region (Fragment).
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Q65ZR6;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
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21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
Pheavy chain V region J558.
Mus musculus (Mouse)
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SMR; P01756; 1-117.
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                                                                                                                                                                                                                                     NCBI_TaxID=10090;
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P01757;
                                                                      HV12 MOUSE
P01756;
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SEQUENCE
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A STEADERLY ENGINE SAUCHANGE.

A STRAINSEVENCY.

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A STRAINSEVENCY.

A Altechul S.F., Zeeberg B.A., Grouse L.H., Derge J.G.,

A Altechul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

A Altechul S.F., Zeeberg B. Buctow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

B Diatchenko L., Marusina K., Farmer A.A., Rubin G.H., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Raha S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

A Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Mitting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Krzywinski M.I., Skalaka U., Smailus D.E.,

Butterfield Y.S.N., Ryzwinski M.I., Skalaka U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

""Generation and initial analysis of more than 15,000 full-length human
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                                                                                                                                    1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             20 BIQLHQSGPELVKPGTSVKMSCKASGYTFTNYYMHWVRQSHGKSLEWIGYIYPNSGATSY 79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            80 NQKFKGKATLIVDKSSTTAYMELRSLISDDSAVYYCARGDLRIGLFDYWGQGTTLIVSS 138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           61 DONFKGKATLIVDKSSTTAFMHLNSLTSDDSAVYFCAR-DVTTAL-DFWGQGTTLTVSS 117
                                                                                                                                                                                 61 DONFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
                                                                                                                                                                                                    1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi,
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
                                                                                      Gaps
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                                                76.2%; Score 470; DB 2; Length 134; 75.2%; Pred. No. 4.4e-39; ive 14; Mismatches 15; Indels
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Submitted (MAY-2005) to the EMBL/GenBank/DDBJ databases.
EMBL; BC096462; AAH96462.1; -; mRNA.
NON_TER 1 1 SQUENCE 134 AA; 14908 MW; 1852D86D26FC7567 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hypothetical protein.
SEQUENCE 483 AA; 52436 MW; 368E7BEE6B6DE9EF CRC64;
                                                                                                                                                                                                                                                                                                                                                     Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        76.2%; Score 470; DB 2; 76.5%; Pred. No. 1.8e-38;
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nes 91; Conservative 12; Mismatches
                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                    Created)
                                                                                                                                                                                                                                                                                                                               13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, 13-SEP-2005 (TrEMBLrel. 31, Hypothetical protein. Mus musculus (Mouse).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN=FVB/N; TISSUE=Colon;
                                                               Best Local Similarity 75.2%
Matches 88; Conservative
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Best Local S:
Matches 91
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This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                heavy chain constant region domains.";
Biochemistry 21:5415-5424(1982).
--- MISCELLANEOUS: The sequence of the light chain of this IgM myeloma protein has also been determined.
--- MISCELLANEOUS: This protein binds dextran.
--- SIMILANETY: Contains 1 Ig-like (Immunoglobulin-like) domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVTTALDFWGQGTTLTVSS 117
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Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Kehry M.R., Fuhrman J.S., Schilling J.W., Rogers J., Sibley C.H., Hood L.E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "Complete amino acid sequence of a mouse mu chain: homology among
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1.
Glycoprotein; Immunoglobulin domain;
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N-linked (GlcNAc. . .) (complex).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    75.0%; Score 463; DB 1; Length 117; 74.4%; Pred. No. 1.9e-38; ive 13; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                      PROTEIN SEQUENCE, AND CARBOHYDRATE-LINKAGE SITE ASN-55.
MEDLINE-83075344; PubMed=6816276;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA; 12983 MW; 3CF8ACE4BE447E41 CRC64;
                                                         21-JUL-1986 (Rel. 01, Created)
21-JUL-1986 (Rel. 01, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 heavy chain V region MOPC 104E.
   117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    117 AA
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InterPro; IPR003596; Ig_v.
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PROSITE; PS50835; IG LIKE;
Direct protein sequencing;
Immunoglobulin V region.
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STANDARD;
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Scheetz T.E.

Casavant T.L.,

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84; Conservative
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Q91WR1;
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Name=Igh-VJ558;
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                                                                                                                                                                                                                                                                                               This Swiss-Prot entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outestation the European Bioinformatics Institute. There are no restrictions on its use as long as its content is in no way modified and this statement is not
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                             TISSUE-Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.

Expression driven by an MMTV-LTR enhancer.;

MEDLINE-22388257; PubMed=12477932; DOI=10.1073/pnas.24503899;

Straubberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

Altechul S.F., Zeeberg B., Buetow K.H., Schemen C.M., Schuler G.D.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  74.6%; Score 460; DB 1; Length 117; 74.4%; Pred. No. 3.8e-38;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           117 AA; 13025 MW; 292E2AF4BE447E41 CRC64;
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01-0CT-2003 (TrEMBLrel. 25, Last sequence update)
01-MAX-2004 (TrEMBLrel. 26, Last annotation update)
Hypothetical protein Al324046.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DitterPro; IPR00110; Ig-like.
InterPro; IPR003596; Ig_v.
SWART; SW00406; Igv.
SWART; PSSO835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin domain; Immunoglobulin V region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Best Local Similarity 74.4%; Pred. No. 3.8e-
Matches 87; Conservative 13; Mismatches
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By similarity.
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                                                                            MEDLINE-80078170; PubMed-6765983;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Q7TMK1 MOUSE PRELIMINARY;
Q7TMK1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                     PIR; A26242; MHMSJ5.
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NUCLEOTIDE SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01751; 1NQB.
SMR; P01757; 1-117.
                NCBI_TaxID=10090;
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NON TER
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Brownetein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McKernen K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Sanchez J., Hulthing M., Madan A., Rotteman M., Madan A., Rouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Schnein J.S., Jones S.J.M., Marza M.A., Schein J.E., Schnerch A., Schein J.E., Jones S.J.M., Marza M.A., "Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          20 EVQLQQSGPELVKPGASVKISCKASGYTFTGYYM#VKQSHGKSLEWIGLVNPSNGDTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sclurognathi;
Muridae; Murinae; Mus.
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NUCLEOTIDE SEQUENCE.
NUCLE 22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEOTIDE SEQUENCE.
STRAIN=CZECH II;
TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
Expression driven by an MMTV-LTR enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Expression carrows a Strausberg R.;

L. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

R. Submitted (AUG-2003) to the EMBL/GenBank/DDBJ databases.

R. RISSP PO1865; 1KB5.

R. GO; GO:0003823; F:antigen binding; IEA.

R. InterPro; IPR003597; Ig.-1.

R. InterPro; IPR003506; Ig.-1.

R. InterPro; IPR003106; Ig.-1.

R. InterPro; IPR003106; Ig.-1.

R. SWART; SW00406; ICV: 1.

DR. PROSITE; PSS0835; IG. LIKE; 4.

DR. PROSITE; PSS0835; IG. LIKE; 4.

DR. PROSITE; PS00290; IG. MHC: Immunoglobulin domain.

K. Hypothetical protein; Immunoglobulin domain.

S. SEQUENCE 470 AA; 51728 MW; 6D9084DF896BB090 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  72.4%; Score 447; DB 2; Length 470; 69.4%; Pred. No. 3.6e-36; ive 16; Mismatches 17; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
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TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     and mouse
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Altechul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heieh F.,
Distchenco L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
B. Stapleton M., Soares M.B., Bonaldo M.F., Casavint T.L., Scheetz T.E.,
B. Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
B. Bosak S.A., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
B. Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunarathe P.H.,
Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
B. Nilalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,
Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
B. Hakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
B. Butterfield Y.S. M., Krzywinski M.I., Skalska U., Smailus D.E.,
M. Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
"Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 DONFKGKATLITVDKSSTTAFMHLNSLTSDDSAVYFCARDVT-----TALDFWGQGTTL 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20 EVQLQQSGPELVKPGASVKLSCKASGYTITDYYVNWVKQSHGKSLEMIGDINPYNGGTSY 79
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus.
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Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
EMBL, BC013539; AAH13539.1; -; mRNA.
EMBL; BC013539; AAH13539.1; -; mRNA.
EMSEP; D01751; 1A600000021155; Mus musculus.
MOI; MGI:96486; Igh-VJ558.
MOI; MGI:96486; Igh-VJ558.
TOCO03823; F:antigen binding; IEA.
InterPro; IPR00110; Ig-like.
InterPro; IPR003597; Ig_C1.
InterPro; IPR003597; Ig_V.
Fram; PF07654; C1-8et; 2.
EMART; SM00406; IGV; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
71.7%; Score 442.5; DB 2; Length 'Best Local Similarity 68.5%; Pred. No. 1.1e-35;
Matches 85; Conservative 14; Mismatches 18; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                              and mouse cDNA sequences.";
Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002),
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Last annotation update)
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PROSITE; PS00290; IG MHC; UNKNOWN 2.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STRAIN=FVB/N; TISSUE=Kidney;
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QEPJA7;
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SEOUENCE 488 AA; 5
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06 PJA7 MOUSE
AC 06 PJA7 MOSE
DT 05 - JUL - 20
DE HYPOCHEC:
GN MUS muse
CC Bukaryote
CC Musmalia,
CC Musmalia,
CC MUSHIT TAX;
RN NUCLEOTII
RC STRAIN-CI
          RAPARA RA
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Expression driven by an WMTV-LTR enhancer;

W Expression driven by an WMTV-LTR enhancer;

W Strausberg R.L., Fealgold E.A., Grouse L.H., Derge J.G.,

Rausberg R.L., Fealgold E.A., Grouse L.H., Derge J.G.,

Rausner R.D. (Collins F.S., Wagner L., Schemen C.M., Schuler G.D.,

A Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

A Hopkins R.F., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

A Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

R Raha S.S., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

R Hillon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Allslan D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Allslan D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A.,

R Allslan D.K., Muzny D.M., Sodergren B.D., Dickson M.C.,

R Bakesly R.W., Touchman J.W., Green E.D., Dickson M.C.,

R Rodriguez A.C., Grimwood J.S., Schmutz J., Myers R.M.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,

R Gehnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

R Generation and initial analysis of more than 15,000 full-length human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      80 NQKFKGKATLIYUDKSSSTAYMELRSLISEDSAVYYCARGYISYYSYDHYFDYWGQGTTIT 139
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TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Whtl model.
Expression driven by an MMTV-LTR enhancer.;
Strausberg R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         .
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REMEL, BC018535, AAH18535.1; -; mRNA.

RISSP, P01865; IKB5.

R MGI; MGI:96443; ISB-1a.

R GO; GO:0003823; F:antigen binding; IEA.

R InterPro; IPR001359; Ig.

R InterPro; IPR00110; Ig-1ike.

R InterPro; IPR00110; Ig-Ai.

R InterPro; IPR003597; Ig_C1.

R InterPro; IPR003597; Ig_C1.

R InterPro; IPR003597; Ig_C1.

R InterPro; IPR003597; Ig_C1.

R SWART; SW00409; IGG. 2.

R SWART; SW004009; IGG. 2.

R SWART; SW00400; IGG.; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     52299 MW; 165169C23D55D4AB CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).
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Last sequence update)
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PROSITE; PS00290; IG_MHC; UNKNOWN_1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hypothetical protein. SEQUENCE 472 AA; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         140 VŠŠ 142
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QBVIJ1 MOUSE
1D QBVIJ1_MC
AC QBVIJ1,
DT 01-MAR-2C
DT 01-MAR-2C
DT 01-MAR-2C
DT 01-MAR-2C
DT 01-MAR-2C
DT 01-MAR-2C
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DONFKGKATLIVDKSSTTAFMHINSLTSDDSAVYFCA----RDVTTALDFWGQGTTLIVS 116
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EVOLOQSGPELVKPGASVKISCKASGYTFTDYYMNWVKQSHGKSLEWIGDINPNNGGTSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 BIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EVQLQQSGPELEKPGASVKISCKASGYSFTGYNMNWVKQSNGKSLEWIGNIDPYYGGTSY
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                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1; Length 118;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-0CT-2003 (TrEMBLrel. 25, Last annotation update)
Pterin-mimicking anti-idiotope heavy chain variable region
                                                                                                                                                                                                                                                                                                                                                                                                              70.3%; Score 433.5; DB 1; Length 70.3%; Pred. No. 1.7e-35; ive 13; Mismatches 21; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUCLEOTIDE SEQUENCE.
Atkin J.D., lape A., Jennings I.G., Horaitis O., Cotton Submitted (SEP-2000) to the EMBL/GenBank/DDBJ databases EMBL, #73107936, #AL09420.1; -; Genomic_DNA.
HSSP; P01791; INQB.
SWR; Q920E8; 1-120.
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                                                                                                                                                                                                                                                                                                                                                        12934 MW; 94F7BEE4C762A018 CRC64;
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
SNART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Direct protein sequencing; Immunoglobulin V region.
I 98 V segment.
REGION 99 104 D segment.
REGION 105 118 J segment.
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                                                                                                                                                                                             V segment.
D segment.
J segment.
By similarity.
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1D Q58E61 MOUSE PRELIMINARY; PRT;
AC Q58E61,
DT 10-MAY-2005 (TrEMBLrel. 30, Created)
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InterPro; IPR003596; Ig_v.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity 70.3% tes 83; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l Similarity 68.3%
82; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q920E8 MOUSE PRELIMINARY;
Q920E8;
                                                                                                                                                                                                                                104
118
96
118
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105 1
22
118 1
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NON TER
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                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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Matches
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092088 MOD
10 00208
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DT 01-DE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 DQNFKGKATLTVDKSSTTAFMHLNSLTSDDSAVYFCARDVT-----TALDFWGQGTTLT 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         61 SQKFKDKATLIVDKSSRTAYMQLNSLISEDSAVYYCARDYTYYTYDEGCFAYWGQGILVT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 8
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                                                                                                                                                                                                                                                                                                            Michael M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S., Wicch M.K., Alexander A.L., Pippen A.M., Pisetsky D.S., Gilkeson G.S., "Differences in V kappa gene utilization and VH CDR3 sequence among anti-DNA from C3H-Dr mice and lupus mice with nephritis."; Eur. J. Immunol. 26:2225-2233(1996).

EMBL, US9154; AAB02916.1; -; mRNA.

EMBL, US9154; AAB02916.1; -; mRNA.

ENSEMDL, ENSWUSGO0000057521; Mus musculus.

InterPro; IPR007110; Ig-like.

InterPro; IPR007110; Ig-like.

MANAMARCA.TG., 19.V.
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Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muroidea; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MEDLINE-84182519; Pubmed-6201362;
Dildrop R., Bovens J., Siekevitz M., Beyreuther K., Rajewsky K.;
"A V region determinant (idiotope) expressed at high frequency in B
"Imphocytes is encoded by a large set of antibody structural genes.";
EMBO J. 3:517-523(1984).
                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Euarchontoglires; Glires; Rodentia; Sciurognathi;
Muridae; Murinae; Mus.
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9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    123 AA; 13806 MW; CC0037A806E9911E CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
10-MAY-2005 (Rel. 47, Last annotation update)
19 heavy chain V region AC38 205.12.
Mus musculus (Mouse).
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                                                                                                                                                                                                                                                                STRAIN=C3H/HeJ-lpr/lpr;
MEDLINE=96409289; PubMed=8814271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMART; SM00406; IGv; 1.7
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STANDARD;
                                            musculus (Mouse)
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HSSP; P01751; 1NQB.
SMR; P06330; 1-118.
                                                                                                                                                                                                                                NUCLEOTIDE SEQUENCE
                                                                                                                                                                 NCBI_TaxID=10090
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P06330;
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HV51_MOUSE

RESULT 12

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                                                                                                                                                                                                                                                                      Expression driven by an NMTV-LTR enhancer.;

Expression driven by an NMTV-LTR enhancer.;

MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

Ratusberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,

Ratusherg R.L., Zeeberg B., Bactow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Bactow K.H., Schaefer C.F., Bhat N.K.,

Mopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Haieh F.,

A stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Frange C.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malled J.J., Hulyk S.W.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Nilalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Radesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Rotiguez A.C., Grimwood J., Schmutz J., Myers R.M.,

Butterfield Y.S. N., Krzywinski M.I., Skalska U., Smailus D.B.,

Butterfield S., Schein J.E., Jones S.J.M., Marra M.A.,

Roderzation and initial analysis of more than 15,000 full-length human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               20 EVQLQQSGAELVKPGASVKISCKASGYTFNDYNMDWYKQSHGRSLEWIGNINPNYDSTIY 79
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                                                                                                      Eukaryota, Metazoa, Chordata, Craniata, Vertebrata, Euteleostomi;
Mammalia, Eutheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinae, Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 EIQLQQSGPELVKPGASVQVSCKTXGYSFTDYNVYWVRQSHGKSLEWIGYIDPYNGITIY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                             TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wntl model.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TISSUE=Mammary tumor metastatized to lung. MMTV-LTR/Wnt1 model. Expression driven by an MMTV-LTR enhancer.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 485;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | Submitted (MAR-2019ct) | Submitted (MAR-2019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Indels
    Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     68.2%; Score 420.5; DB 2; 65.6%; Pred. No. 1.7e-33; ive 17; Mismatches 20;
10-MAY-2005 (TrEMBLrel. 30, 10-MAY-2005 (TrEMBLrel. 30,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   and mouse cDNA sequences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 65.57
Best Local Similarity 65.57
Conservative
                                        Igh-VJ558 protein.
Name=Igh-VJ558;
Mus musculus (Mouse)
                                                                                                                                                                                                                SEQUENCE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUCLEOTIDE SEQUENCE.
                                                                                                                                                                           NCBI TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN=Czech II;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NIH MGC Project,
                                                                                                                                                                                                                                       STRAIN=Czech II
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             116 SS 117
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TISSUE-Thymus;

WEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RETARUBDENG R.L., Feingold B.A., Grouse L.H., Derge J.G.,

RETARUBDENG R.L., Zeeberg B., Barcow K.H., Schaefer C.F., Bhat N.K.,

Altschul S.F., Zeeberg B., Bucrow K.H., Schaefer C.F., Bhat N.K.,

Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,

Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,

Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,

Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,

Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

Rahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,

Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,

Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,

""" "Generation and initial analysis of more than 15,000 full-length human
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Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

Submitted (MAR-2005) to the EMBL/GenBank/DDBJ databases.

I FUNCTION: Beta-2-androgalobulin is the beta-chain of major histocompatibility complex class I molecules (By similarity).

Interprojection (Brools) (By similarity).

SMR; GEBLZ; 21-454.

RINGELLUIAR LOCATION: Secreted (By similarity).

RINGELLUI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus (Rat).
Bukaryota, Metazoa, Chordata, Craniata, Vertebrata, Buteleostomi,
Mammalia, Butheria, Euarchontoglires, Glires, Rodentia, Sciurognathi,
Muroidea, Muridae, Murinaè, Rattus.
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SEQUENCE 458 AA; 50161 MW; A0A61DCDD2CA433E CRC64;
                                                                                                                                                                                                                                   Last sequence update)
Last annotation update)
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                       458 AA
                                                                                                                                                                    Created)
               PRT;
                                                                                                                                                            10-MAY-2005 (TrEMBLrel. 30, 10
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OSBJZZ RAT PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUCLEOTIDE SEQUENCE.
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                                                                                                                                                                                                                                                                                                                                                                                        LOC367586 protein.
Name=LOC367586;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=10116;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TISSUE=Thymus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 80
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Search completed: April 18, 2006, 13:39:33 Job time : 231 secs

Protein Sequence Searches - February 2005

All of the sequence databases on ABSS have recently been updated.

- permanent accession numbers. The new UniProt record may not contain the previous temporary numbers from the most recent version of UniProt. These sequences have been assigned new Please note that the curators of the UniProt database have purged some temporary accession
- extension .rup) that can no longer be found in the database, the permanent record with the new accession number can be found by searching the old accession number in the UniProt Protein If you encounter an accession number from an older search run against UniProt (results file

http://www.pir.uniprot.org/database/archive.shtml

If you have any questions regarding this information or your results, please contact any STIC searcher.

members of the public who may encounter UniProt temporary accession When submitting sequence search results for scanning into IFW, please include a copy of this attachment to assist any future Examiners or numbers. THIS PAGE LEFT BLANK